

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 13:12:36 ; Search time 37 Seconds
(without alignments)
257.826 Million cell updates/sec

Title: US-09-856-320A-2_COPY_53_282

Perfect score: 1263
Sequence: 1 KIKGFCECKPHSQPWQALF.....GVYTKCKYVDWIQETMKNK 230

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1263	100.0	250	1	KLKB_HUMAN
2	739	58.5	250	1	KLK9_HUMAN
3	689	54.6	260	1	NRPN_RAT
4	686	54.3	260	1	NRPN_MOUSE
5	684	54.2	236	1	KLKF_HUMAN
6	683	54.1	260	1	KLKB_HUMAN
7	677.5	53.6	277	1	KLKD_HUMAN
8	649.5	51.4	293	1	KLK5_HUMAN
9	623	49.3	251	1	KLKE_HUMAN
10	610.5	48.3	261	1	KLK1_RAT
11	608	48.1	248	1	KLKC_HUMAN
12	605.5	47.9	261	1	KLK7_RAT
13	600.5	47.5	261	1	KLK3_MOUSE
14	596.5	47.2	263	1	KLKR_PRANA
15	596	47.2	248	1	TRV3_CHICK
16	593	47.0	246	1	TRV2_RAT
17	590.5	46.8	261	1	KLK8_RAT
18	590	46.7	238	1	TRV3_SALSA
19	589	46.6	246	1	TRV1_RAT
20	586.5	46.4	259	1	KLKC_RAT
21	582.5	46.1	261	1	KLK2_HUMAN
22	582.5	46.1	261	1	KLK9_MOUSE
23	579	45.8	231	1	TRYP_PIG
24	579	45.8	231	1	KLK6_HUMAN
25	575.5	45.6	246	1	KLK_PIG
26	573	45.4	246	1	TRV2_MOUSE
27	572.5	45.3	259	1	KLK2_RAT
28	571.5	45.2	261	1	TRV2_CHICK
29	570	45.1	247	1	KLK1_MOUSE
30	569.5	45.1	244	1	TRV2_CANFA
31	569.5	45.1	261	1	KLK1_RAT
32	567	44.9	262	1	KLK6_MOUSE
33	566	44.8	243	1	TRV1_BOVIN

34	563	44.6	248	1	TRV1_CHICK	Q90627 gallus gall
35	561.5	44.5	257	1	KLK1_MACFA	O07276 macaca fasc
36	561.5	44.5	261	1	KLKB_MOUSE	P15946 mus musculu
37	559	44.3	244	1	TRV2_XENLA	P70059 xenopus lae
38	559	44.3	248	1	TRV2_CHICK	Q90628 gallus gall
39	558	44.2	243	1	TRV1_XENLA	P19799 xenopus lae
40	558	44.2	247	1	TRV2_BOVIN	Q29463 bos taurus
41	556.5	44.1	261	1	KLK3_HUMAN	P08426 homo sapien
42	555	43.9	247	1	TRV3_RAT	P08426 rattus norv
43	554.5	43.9	231	1	TRV2_SALSA	P35032 salmo salar
44	554.5	43.9	247	1	TRV4_RAT	P12788 rattus norv
45	554	43.9	258	1	KLK1_PAPUA	Q28773 papio hamad

ALIGNMENTS

RESULT 1	KLKB_HUMAN	STANDARD;	PRT;	250 AA.
ID	KLKB_HUMAN	Q90627		
AC	Q90627	Q75837; Q9NS65;		
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Kallikrein II precursor (EC 3.4.21.-) (Hypostasin) (Trypsin-like protease).			
GN	KLK11 OR PRSS20 OR TLSP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Hippocampus;			
RX	MEDLINE=98438738; PubMed=9765601;			
RA	Yoshida S., Taniguchi M., Suenoto T., Oka T., He X.P., Shiosaka S.; "cDNA cloning and expression of a novel serine protease, TLSP.";			
RT	Biochim. Biophys. Acta 1399:225-228(1998).			
RL	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1 AND 2).			
RC	TISSUE=Hippocampus, and Prostate;			
RX	MEDLINE=20329229; PubMed=10872828;			
RA	Mitsu S., Yamada T., Okui A., Komihama K., Uemura H., Yamaguchi N.; "A novel isoform of a kallikrein-like protease, TLSP/hypostasin, (PRSS20), is expressed in the human brain and prostate.";			
RT	Biochem. Biophys. Res. Commun. 272:205-211(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=20130117; PubMed=10662548;			
RA	Yousef G.M., Scortilas A., Diamandis E.P.; "Genomic organization, mapping, tissue expression, and hormonal regulation of trypsin-like serine protease (TLSP/PRSS20), a new member of the human kallikrein gene family.";			
RT	Genomics 63:88-96(2000).			
RL	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=20510030; PubMed=11054574;			
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paepker B., Wang K.; "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";			
RT	Gene 257:119-130(2000).			
RL	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V., Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stiliwagen S., Phan H., Velasco N., Do U., Regala W., Terry A., Brower A., Gaines J., Dangnan L., Ertler A., Christensen M., Georgescu A., Avila J., Liu S., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B., Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.; "Sequence analysis of chromosome 19q13.4.";			
RT				

Aug 20

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Testis;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: POSSIBLE MULTIFUNCTIONAL PROTEASE. EFFICIENTLY CLEAVES
 CC B2-PHE-ARG-4-METHYLCOOMARYL-7-AMIDE, A KALLIKREIN SUBSTRATE, AND
 CC WEAKLY CLEAVES OTHER SUBSTRATES FOR KALLIKREIN AND TRYPSIN.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SKIN AND PROSTATE. ISOFORM
 CC 1 IS EXPRESSED PREFERENTIALLY IN BRAIN; ISOFORM 2 IN PROSTATE.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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 CC -----
 DR EMBL: AB012917; BAA33404.1; ALT_INIT.
 DR EMBL: AB013730; BAA88713.1; -
 DR EMBL: AB041036; BAA96797.1; -
 DR EMBL: AF164623; AAD47815.1; -
 DR EMBL: AF243527; AAG33364.1; -
 DR EMBL: AC011473; AAG33257.1; -
 DR EMBL: BC022068; AAR22068.1; -
 DR HSSP: P00763; 1DPO.
 DR MEROPS: S01.257; -
 DR Genew; HGNC:6359; KLK11.
 DR MIM; 604434; -
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser.protease_Try.
 DR Pfam: PFO0089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR KMW Hydrolyase; Serine protease; Glycoprotein; Signal; Zymogen;
 KM Alternative splicing.
 FT SIGNAL 1 18
 FT PROPEP 19 21
 FT CHAIN 22 250
 FT ACT_SITE 62 62
 FT ACT_SITE 110 110
 FT ACT_SITE 203 203
 FT DISULFID 28 163
 FT DISULFID 47 63
 FT DISULFID 135 237
 FT DISULFID 142 209
 FT DISULFID 174 188
 FT DISULFID 199 224
 FT CARBOHYD 99 99
 FT CARBOHYD 165 165
 FT CARBOHYD 181 181
 FT CARBOHYD 210 210
 FT VARSPLIC 1 1
 SQ SEQUENCE 250 AA; 27466 MW; 192D910BDCD7A56 CRC64;
 Query Match 100.0%; Score 1263; DB 1; Length 250;
 Best Local Similarity 100.0%; Pred. No. 7; le-109;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIKGECPKPHSQPQWALFEKTRILCGATLLAPRWMLTAHCLRPRTYVHLGHNLOKE 60
 DB 21 KIKGECPKPHSQPQWALFEKTRILCGATLLAPRWMLTAHCLRPRTYVHLGHNLOKE 80

QY 61 EGCQRTATSEPPHPGFNNSLPKKDRNDIMLYKASPVSTIMAWRPLTLSSRCVYACT 120
 DB 81 EGCQRTATSEPPHPGFNNSLPKKDRNDIMLYKASPVSTIMAWRPLTLSSRCVYACT 140
 QY 121 SCLSIGWSTSPQLRPHRLRCANITIIIEHOKCENAPENITDTWVCASVGGGDSQ 180
 DB 141 SCLSIGWSTSPQLRPHRLRCANITIIIEHOKCENAPENITDTWVCASVGGGDSQ 200
 QY 181 GDSGGLVNCQSIQIGISWQDPCATITRKPGYTVKCKYVDWIQETMKN 230
 DB 201 GDSGGLVNCQSIQIGISWQDPCATITRKPGYTVKCKYVDWIQETMKN 250
 RESULT 2
 KIK9_HUMAN
 ID KIK9_HUMAN STANDARD; PRT; 250 AA.
 AC 09UKQ9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Kallikrein 9 precursor (EC 3.4.21.-) (Kallikrein-like protein 3) (KLK-13).
 GN KIK9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20118156; PubMed=10652563;
 RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
 RT Identification of novel human kallikrein-like genes on chromosome
 RT 19q13.3-q13.4.
 RL Anticancer Res. 19:2843-2852(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20247258; PubMed=10783266;
 RA Yousef G.M., Diamandis E.P.;
 RT "The expanded human kallikrein gene family: locus characterization and
 RT molecular cloning of a new member, KLK-13".
 RL Genomics 65:184-194(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20510030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
 RA Moss P., Paepfer B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region.";
 RL Gene 257:119-130(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Vissanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwogen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J.,
 RA Danganan L., Erikheim M., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.;
 RT "Sequence analysis of chromosome 19q13.4.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- TISSUE SPECIFICITY: SKIN, THYMUS, TRACHEA, CEREBELLUM AND SPINAL
 CC CORD.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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CC EMBL: AF135026; AAD26427.2;
DR EMBL: AF243527; AAG33362.1;
DR HSSP: AC011473; AAG23255.1;
DR HSSP: P00763; IDPO.
DR MEROPS: S01.307; -.
DR Genew: HGNC:6370; KIK9.
DR MIM: 605504; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin.1.
DR PRINTS: PR00722; CHYMOTRYPsin.
DR SMART: SM00020; Tryp_SPC.1.
DR PROSITE: PS50240; TRYPsin_DOM.1.
DR PROSITE: PS00134; TRYPsin_HIS.1.
DR PROSITE: PS00135; TRYPsin_SER.1.
KM Hydroxylase; Serine protease; Glycoprotein; signal.
FT SIGNAL 1
FT CHAIN 16 250
FT ACT_SITE 63
FT ACT_SITE 111 111
FT ACT_SITE 204 204
FT DISULFID 29 164
FT DISULFID 48 64
FT DISULFID 136 238
FT DISULFID 143 210
FT DISULFID 175 189
FT DISULFID 200 225
FT CARBOHYD 131 131
FT CARBOHYD 166 166
FT CARBOHYD 211 211
SQ SEQUENCE 250 AA; 27512 MW; F2785245B063E9B8 CRC64;

Query Match 58.5%; Score 739; DB 1; Length 250;
Best Local Similarity 58.1%; Pred. No. 8.8e-61;
Matches 133; Conservative 35; Mismatches 61; Indels 0; Gaps 0;

QY 1 RIINGECKPHSPQWQALFEKTRILCGATLIARWLLTAHCLKPRYVHLGQHNLOKE 60
DB 22 RALGAEBCRPNSQPMWQAGLFHLTRLCGATLISDRWLLTAHCKRPYLAWVLGSHHLMKW 81
QY 61 EGCQRTATSEFPHPGFNSLPKNDHNDIMLVKMASPVSIWAVRPLTLSSRCVYAGT 120
DB 82 EGPQLFRVYDFPHGFNSLPKNDHNDIMLVKMASPVSIWAVRPLTLSSRCVYAGT 141
QY 121 SCLISGSGSTSPQRLPHTLRCANITITIEHOKENAYPGNITPPMVCASVQEGKXSCQ 180
DB 142 QCLISGSGVAVSPKALFPVTLQCANISILENKLCHMAVPGHISDMLCAGIMEGRSCQ 201
QY 181 GDSGGLVNCVDSLGIIISGQDPCATIRKPGVYTKVCKYVDWIQETMKN 229
DB 202 GDSGGLVNCVDSLGIIISGQDPCATIRKPGVYTKVCKYVDWIQETMKN 250

RESULT 3
NRPN_RAT STANDARD; PRT; 260 AA.
ID NRPN_RAT
AC 088780;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neutropin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine
  protease 1).
GN KIK8 OR PRSS19 OR NRPN OR BSP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer; TISSUE=Brain;
RX MEDLINE=98389725; PubMed=9722524;
RA Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;

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RT "Serine proteases in rodent hippocampus."
RL J. Biol. Chem. 273:23004-23011(1998).
CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
CC HIPPOCAMPAL PLASTICITY. HAS A STRONG PROTEOLYTIC ACTIVITY AGAINST
CC FIBRONECTIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-.
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- TISSUE SPECIFICITY: RESTRICTED TO HIPPOCAMPUS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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CC or send an email to license@isb-sib.ch).
CC EMBL: AJ005641; CA006643.1;
DR HSSP: Q61955; INPM.
DR MEROPS: S01.244; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin.1.
DR PRINTS: PR00722; CHYMOTRYPsin.
DR SMART: SM00020; Tryp_SPC.1.
DR PROSITE: PS50240; TRYPsin_DOM.1.
DR PROSITE: PS00134; TRYPsin_HIS.1.
DR PROSITE: PS00135; TRYPsin_SER.1.
KM Hydroxylase; Serine protease; Glycoprotein; zymogen; signal.
FT SIGNAL 1
FT PROPEP 29 32
FT CHAIN 33 260
FT ACT_SITE 73 73
FT ACT_SITE 120 120
FT ACT_SITE 212 212
FT DISULFID 39 173
FT DISULFID 58 74
FT DISULFID 145 246
FT DISULFID 152 218
FT DISULFID 184 198
FT DISULFID 208 233
FT CARBOHYD 110 110
SQ SEQUENCE 260 AA; 28510 MW; 58DF4F0602A0BF75 CRC64;

Query Match 54.6%; Score 689; DB 1; Length 260;
Best Local Similarity 53.3%; Pred. No. 3.6e-56;
Matches 121; Conservative 36; Mismatches 68; Indels 2; Gaps 2;

QY 1 RIINGECKPHSPQWQALFEKTRILCGATLIARWLLTAHCLKPRYVHLGQHNLOKE 60
DB 32 KILGQCKPHSPQWQALFQGERLVGCGVLRWVLTAAHCKKDKSVNLGSHSLQKR 91
QY 61 EGCQRTATSEFPHPGFNSLPKNDHNDIMLVKMASPVSIWAVRPLTLSSRCVYAGT 120
DB 92 DEPEQEIQVARSIQHPFNSSNP-EDSHDMLIRLQNSANLGDVPRIELANLCPKVG 150
QY 121 SCLISGSGSTSPQRLPHTLRCANITITIEHOKENAYPGNITPPMVCASVQEGKXSCQ 180
DB 151 KCLISGSGVAVSPKALFPVTLQCANISILENKLCHMAVPGHISDMLCAGIMEGRSCQ 209
QY 181 GDSGGLVNCVDSLGIIISGQDPCATIRKPGVYTKVCKYVDWIQETMKN 227
DB 210 GDSGGLVNCVDSLGIIISGQDPCATIRKPGVYTKVCKYVDWIQETMKN 256

RESULT 4
NRPN_MOUSE STANDARD; PRT; 260 AA.
ID NRPN_MOUSE
AC 061955;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

```

DE Neurepsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8).
GN KLK8 OR PRSS19 OR NRPN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c; TISSUE=Hippocampus;
RX MEDLINE=95348817; PubMed=7623137;
RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
RA Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;
RT "Expression and activity-dependent changes of a novel limbic-serine
RT protease gene in the hippocampus.";
RL J. Neurosci. 15:5088-5097(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Yoshida S., Hirata A., Inoue N., Shiosaka S.;
RT "Cloning and assignment of mouse neurepsin gene, Prss19 to chromosome
RT 7B4.";
RN Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF N-TERMINUS, AND CHARACTERIZATION.
RC STRAIN-BALB/c; TISSUE=Brain;
RX MEDLINE=98225202; PubMed=9556608;
RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
RA Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;
RT "Characterization of recombinant and brain neurepsin, a
RT plasticity-related serine protease.";
RL J. Biol. Chem. 273:11189-11196(1998).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
RC TISSUE=Hippocampus;
RX MEDLINE=99134351; PubMed=9933620;
RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
RA Shiosaka S., Hakoshima T.;
RT "Crystal structure of neurepsin, a hippocampal protease involved in
RT kindling epileptogenesis.";
RL J. Biol. Chem. 274:4220-4224(1999).
CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
CC HIPPOCAMPAL PLASTICITY. HAS A STRONG PROTEOLYTIC ACTIVITY AGAINST
CC FIBRONECTIN.
CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-
CC -1- ENZYME REGULATION: STRONGLY INHIBITED BY DIISOPROPYL
CC FLUOROPHOSPHATE, LEUPEPTIN AND (4-AMIDINOPHENYL)METHANESULFONYL 1-
CC FLUORIDE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE LIMBIC SYSTEM OF
CC MOUSE BRAIN AND IS LOCALIZED AT HIGHEST CONCENTRATION IN PYRAMIDAL
CC NEURONS OF THE HIPPOCAMPAL CA1-3 SUBFIELDS.
CC -1- MASS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGE=29-260.
CC -1- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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CC -----
DR EMBL, D30785; BAA06451.1; -
DR EMBL, AB032202; BAA92435.1; -
DR PDB, INPM: 23-MAR-99.
DR MEROPS: S01.244; -
DR MGD, MGI:892018; Kik8.
DR InterPro, IPR001314; Chymotrypsin.
DR InterPro, IPR001254; Ser-protease_try.
DR Pfam, PF00089; trypsin. 1.
DR PRINTS, PR00722; CHYMOTRYPSIN.
DR SMART, SM00020; TRYPSIN_SPEC_1.
DR PROSITE, PS50240; TRYPSIN_DOM; 1.

DR PROSITE, PS00134; TRYPSIN_HIS; 1.
DR PROSITE, PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Glycoprotein; Zymogen; Signal;
FT 3D-structure.
FT SIGNAL 1 28 POTENTIAL.
FT PROPEP 29 32
FT CHAIN 33 260
FT ACT_SITE 73 73 NEUROPSIN.
FT ACT_SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 39 173 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 58 74
FT DISULFID 145 246
FT DISULFID 152 218
FT DISULFID 184 198
FT DISULFID 208 233
FT CARBOHYD 110 110
SQ SEQUENCE 260 AA; 28523 MW; B556FEB37CD06E CRC64; N-LINKED (GLCNAC...) (POTENTIAL).
Query Match 54.3%; Score 686; DB 1; Length 260;
Best Local Similarity 52.8%; Pred. No. 6,7e-56;
Matches 121; Conservative 36; Mismatches 70; Indels 2; Gaps 2;
QY 1 RIIRFECRPHSQPNOALFEKTRLLCGATLIPRHULTRAHGLKRYIYHLOHLOKE 60
DB 32 KILEGRECIPLHSQWQAAALFQGERLLCGVLDKRWVLAHAHCKOKYSVRLDHSLSQR 91
QY 61 EGCEQRRATSEPPHPGFNSLPKNDHNDIMLVKNAAPSYITWAVRPLTSSRCVTAGT 120
DB 92 DPEQELQVAGSTQHPCYNNNSN-EDHSHDIMLRQNSNGLDKKPKVQLANLCKRVQ 150
QY 121 SCLISGWSSTSPQLRPLPTLRCANITLIEHOCENAYPCNITDYMVCASVQEGGKDSQ 180
DB 151 KCIISGSGTWTSPQENFPTLNCAEVYKISQNKCEBAPGKITEGWACAG-SSNGADTQ 209
QY 181 GDSGGLVYCNOSLGITISNODPCATRRKGVYTKYCKVYDQMKN 229
DB 210 GDSGGLVYCDMGLGITWSGDPCKGRPKRVYTKICRYTWIKTKMDN 258
RESULT 5
KIKF_HUMAN
ID KIKF_HUMAN STANDARD; PRT; 256 AA.
AC Q9H2R5; Q9H2R6; Q9H2R4; Q9H2R3; Q9H2R3; Q15358;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kallikrein 15 precursor (EC 3.4.21.-) (Aco protease).
GN KLK15.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RX PubMed=11010966;
RA Yousef G.M., Scorilas A., Jung K., Ashworth L.K., Diamandis E.P.;
RT "Molecular cloning of the human kallikrein 15 gene (KLK15). Up-
RT regulation in prostate cancer.";
RL J. Biol. Chem. 276:53-61(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20510030; PubMed=11054574;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepel B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [3]
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94289486; PubMed=8018728;
RA Dhanich M.E., Spiess M.;

RT "A novel serine proteinase-like sequence from human brain.";
 RL Biochim. Biophys. Acta 1218:225-228(1994).
 CC -1- FUNCTION: Protease whose physiological substrate is not yet known.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- ALTERNATIVE PRODUCTS: 4 isoforms: 1 (shown here), 2, 3 and 4; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also
 CC expressed in the prostate, salivary, and adrenal glands and in the
 CC colon testis and kidney.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC
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 CC
 CC EMBL: AF242195; AAC09469.1; -;
 CC EMBL: AF242195; AAC09470.1; -;
 CC EMBL: AF242195; AAC09471.1; -;
 CC EMBL: AF242195; AAC09472.1; -;
 CC EMBL: AF243527; AAC33354.1; -;
 CC EMBL: X75363; CA53145.1; ALT_SEQ.
 CC HSP: P00763; IDPO.
 CC MEROPS: S01.081; -;
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR001254; Ser. protease_Try.
 CC Pfam: PF00089; trypsin_1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC SMART: SM00020; TRYPSIN_1.
 CC PROSITE: PS50240; TRYPSIN_DOM; 1.
 CC PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC PROSITE: PS00135; TRYPSIN_SER; FALSE NEG.
 CC DR Hydroxylase: Serine protease; Glycoprotein; signal; zymogen;
 CC KM Alternative splicing.
 CC FT SIGNAL 1 16
 CC FT PROPEP 17 21
 CC FT CHAIN 22 256
 CC FT ACT_SITE 62 62
 CC FT ACT_SITE 106 106
 CC FT ACT_SITE 209 209
 CC FT CARBOHYD 171 171
 CC FT CARBOHYD 232 232
 CC FT VARSPPLIC 122 256
 CC FT VARSPPLIC 122 256
 CC FT VARSPPLIC 161 161
 CC FT VARSPPLIC 162 256
 CC FT CONFLICT 147 160
 CC SQ SEQUENCE 256 AA; 28087 MW; B5EBF8D6022786B5 CRC64;
 Query Match 54.2%; Score 684; DB 1; Length 256;
 Best Local Similarity 51.7%; Pred. No. 1e-55;
 Matches 12; Conservative 37; Mismatches 65; Indels 14; Gaps 3;

RESULT 6
 ID K1K8_HUMAN STANDARD: PRT; 260 AA.
 AC 060259; Q9U047; Q9HCB3; Q9U1L9;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neuropilin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Ovasin) (Serine
 DE protease TADG-14) (Tumor-associated differentially expressed gene-14
 DE protein).
 GN K1K8 OR PRS19 OR TADG14 OR NRPN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Hippocampus;
 RX MEDLINE=98372070; PubMed=9714609;
 RT Yoshida S., Taniguchi M., Hirata A., Shiosaka S.;
 RT "Sequence analysis and expression of human neuropilin cDNA and gene.";
 RT Gene 213:9-16(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain;
 RX MEDLINE=99203457; PubMed=10102990;
 RA Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.;
 RA "A novel form of human neuropilin, a brain-related serine protease, is
 RA generated by alternative splicing and is expressed preferentially in
 RA human adult brain.";
 RA Eur. J. Biochem. 260:627-634(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Ovary;
 RX MEDLINE=99413504; PubMed=10485494;
 RA Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H.,
 RA O'Brien T.J.;
 RA "Cloning of tumor-associated differentially expressed gene-14, a novel
 RA serine protease overexpressed by ovarian carcinoma.";
 RA Cancer Res. 59:4435-4439(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Gan L., Gellinas R., Gown A.M., Moss P., Smith R., Wang K.;
 RA "Molecular cloning and characterization of a novel serine protease,
 RA ovasin, a potential molecular marker for ovarian carcinomas.";
 RA Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20510030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCaig J.,
 RA Moss P., Paepker B., Wang K.;
 RA "Sequencing and expression analysis of the serine protease gene
 RA cluster located in chromosome 19q13 region.";
 RA Gene 257:119-130(2000).
 RN [6]
 RP SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).
 RA Lemerding J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 RA Pan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J.,
 RA Danganan L., Frankel M., Attix C., Amico-Keller G., Coffield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carraro A.V.;
 RA "Sequence analysis of chromosome 19q13.4.";
 RA Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RT
 RT -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
 RT HIPPOCAMPAL PLASTICITY.
 CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, IYS-.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2. ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS PREDOMINANTLY EXPRESSED IN THE

[illegible]

CC	EMBL: AF135024; AAD26425.2; -	FT	1	16	POTENTIAL.
DR	EMBL: AC011473; AAG31259.1; - <td>FT</td> <td>76<td>76<td>KALIKREIN 13.</td></td></td>	FT	76 <td>76<td>KALIKREIN 13.</td></td>	76 <td>KALIKREIN 13.</td>	KALIKREIN 13.
DR	EMBL: AL050220; CABG3320.1; ALT_INIT. <td>FT</td> <td>124<td>124<td>CHARGE RELAY SYSTEM (BY SIMILARITY).</td></td></td>	FT	124 <td>124<td>CHARGE RELAY SYSTEM (BY SIMILARITY).</td></td>	124 <td>CHARGE RELAY SYSTEM (BY SIMILARITY).</td>	CHARGE RELAY SYSTEM (BY SIMILARITY).
DR	HSP; P00763; IDPO. <td>FT</td> <td></td> <td></td> <td>CHARGE RELAY SYSTEM (BY SIMILARITY).</td>	FT			CHARGE RELAY SYSTEM (BY SIMILARITY).
DR	MEROPS; S01.306; - <td>FT</td> <td></td> <td></td> <td></td>	FT			
DR	Genew; HGNC:6361; KUK13. <td>FT</td> <td></td> <td></td> <td></td>	FT			
DR	MIM; 605505; - <td>FT</td> <td></td> <td></td> <td></td>	FT			
DR	InterPro: IPR001314; ChymoTrypsIn. <td>FT</td> <td></td> <td></td> <td></td>	FT			
DR	InterPro: IPR001254; Ser_protease_Try. <td>FT</td> <td></td> <td></td> <td></td>	FT			
DR	Pfam: PF00089; trypsin; 1. <td>FT</td> <td></td> <td></td> <td></td>	FT			
DR	PRINTS; PR00722; CHYMOTRYPSIN. <td>FT</td> <td></td> <td></td> <td></td>	FT			
DR	SMART; SM00020; Tryp_Sp; 1. <td>FT</td> <td></td> <td></td> <td></td>	FT			
DR	PROSITE; PS50240; TRYPSIN_DOM. 1. <td>FT</td> <td></td> <td></td> <td></td>	FT			
DR	PROSITE; PS00134; TRYPSIN_HIS. 1. <td>FT</td> <td></td> <td></td> <td></td>	FT			
DR	PROSITE; PS00135; TRYPSIN_SER. 1. <td>FT</td> <td></td> <td></td> <td></td>	FT			
KM	Hydrolase; Serine protease; Glycoprotein; Signal. <td>FT</td> <td></td> <td></td> <td></td>	FT			
FT	SIGNAL	FT	1	16	POTENTIAL.
FT	CHAIN	FT	17	277	KALIKREIN 13.
FT	ACT_SITE	FT	76	76	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	FT	124	124	CHARGE RELAY SYSTEM (BY SIMILARITY).

FT	ACT SITE	218	218	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	DISULFID	42	178	BY SIMILARITY.
FT	DISULFID	61	77	BY SIMILARITY.
FT	DISULFID	157	224	BY SIMILARITY.
FT	DISULFID	189	203	BY SIMILARITY.
FT	DISULFID	214	239	BY SIMILARITY.
FT	CARBOHYD	30	30	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	225	225	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	170	180	UNRETTLOCAN -> GMPHPRWEAP (IN REF. 3).
SO	SEQUENCE	277 AA;	30570 MM;	BA8A9E8DCEB5D542 CRC64;

Query Match	Best local similarity	53.6%	Score 677.5;	DB 1:	Length 277;
Matches 120;	Conservative 41;	Mismatches 65;	Indels 1;	Gaps 1;	

QY	5	GFECRPHSPQWALFEKTRRLGATLLAPRWLLTAHCLKPRYIVHLSQHNLOKEEGCE	64
DB	39	GVTCPRHSPQWQALALVYGRILCGGLVLPKVVLLTAHCLKRGKLVYGLKHALGRVNAE <th>98</th>	98
QY	65	QTRTATESPRHGFNNSLPKNDHRNDIMLVKASPVSTWAVRPLTSL-SRCVTAAGTSL <th>123</th>	123
DB	99	QYREVVAHSIPHEPRRSPTHLNHDHIMLEQLSPVLGXIQTLPLSHNNRLTFGTCTCR <th>158</th>	158
QY	124	ISGWCSTSPQRLRHTLRGANTITIEHQKCNAPGNTTDMWCAVSQEGKDCQCGS <th>183</th>	183
DB	159	VSGWCTTSPVQVNYPRYTLQACANIQLRSDECHQVYPRGKTTDMNLGAKRGKDCQCGS <th>218</th>	218
QY	184	GGPLVCNOSLOGIISMGODPCATIRKPRGYTKVCKYVDIMQETMK <th>228</th>	228
DB	219	GGPLVCNRTLYGIVSMGDFPCGQPRPRGYTVRSKRVLMIRRTIR <th>263</th>	263

RESULT 8	KLKS_HUMAN	STANDARD;	PRT:	293 AA.
AC	Q9Y337; Q9HBC8;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Kallikrein 5 precursor (EC 3.4.21.-) (Stratum corneum tryptic enzyme)			
DE	(Kallikrein-like protein 2) (KLK-L2).			
GN	KLKS OR SCTE.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid:9606;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Stratum corneum;			
RA	MEDLINE=99445563; PubMed=10514489;			
RA	Brattand M., Egeland T.;			
RT	"Purification, molecular cloning, and expression of a human stratum			
RT	corneum trypsin-like serine protease with possible function in			
RT	desquamation.";			
RT	J. Biol. Chem. 274:30033-30040(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=20118156; PubMed=10652563;			
RA	Yousef G.M., Luo L.-Y., Diamandis E.P.;			
RT	"Identification of novel human kallikrein-11-like genes on chromosome			
RT	19q13.3-q13.4.";			
RL	Anticancer Res. 19:2843-2852(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=20510030; PubMed=11054574;			
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McNulty J.,			
RA	Moss P., Paepel B., Wang R.;			
RT	"Sequencing and expression analysis of the serine protease gene			
RT	cluster located in chromosome 19q13 region.";			
RL	Gene 257:119-130(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Ovary;			
RC				

```

RA      Strausberg R.:
RL Submitted (MAY-2001) to the EMBL/Genbank/DDBJ databases.
CC -I- FUNCTION: MAY BE INVOLVED IN DESQUAMATION.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: EXPRESSED IN SKIN, BREAST, BRAIN AND TESTIS.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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DR EMBL; AF168768; AAF03101.1; -
DR EMBL; AF15028; AAD26429.1; -
DR EMBL; AF243527; AAC33358.1; -
DR EMBL; BC008036; AAH08036.1; -
DR HSSP; P00763; IDPO.
DR MEROPS; S01_017; -.
DR Genew; HGNC:6366; KLK5.
DR MIM; 605643; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease TRY.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPE; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 1 293 KALLIKREIN 5.
FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 153 153 CHANGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 245 245 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 73 206 BY SIMILARITY.
FT DISULFID 93 109 BY SIMILARITY.
FT DISULFID 178 279 BY SIMILARITY.
FT DISULFID 185 251 BY SIMILARITY.
FT DISULFID 217 231 BY SIMILARITY.
FT DISULFID 241 266 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 25 56 MISSING (IN REF. 3).
SQ SEQUENCE 293 AA; 32020 MW; D92C92F5609E5946 CRC64;

Query Match 51.4%; Score 649.5; DB 1; Length 293;
Best Local Similarity 50.9%; Pred. No. 1.7e-52;
Matches 118; Conservative 40; Mismatches 67; Indels 7; Gaps 4;

QY 1 RIIFGECKPPSPOPMOA-LFEKTRILGATLLIARWLITFAHCLLPRIYVHLGGHNLOK 59
||| : | : ||||| : | : ||| : | : ||||| | : | : | :
Db 66 RIINSDDDMHTGPQAALLRPNLYCGAVLVHQMVLTAHCKKKFRRLRGHSLSIP 125

QY 60 -EEGCEGTATSEFPHEGFENNSLPNKDRNDIMLVKASPVSTWAVRPLTLSSRCYTA 118
| : | : ||||| : | : ||||| : | : ||||| : | : ||| : | : | :
Db 126 VYESGOOGFQGVKSIPIHPTS----HPGHSDIIIMLIKLRNRIRPKDVRIIVSSHCSDSA 181

QY 119 GTSCILSGWGSTSSPQLPHLTRLCANTITIEHQECENAAVNGNTIDTDVYKASVDGEGDS 178
||| : ||||| : ||| : | : | : ||||| : ||||| : ||| : | : | :
Db 182 GTKCLVASWGTGTSQVVEPVPYLQCLNLSVLSQKCEDEAYPRPDIDTFMCAG-DGAGDS 240

QY 179 CGDGSGGLVGNOSLOGIISGWODCAPITRRPGVTYVKCYVDVIOETMKNN 230
||||| : ||||| : ||||| : ||| : | : ||||| : ||||| : ||||| : |
Db 241 CQGDSGGGVYVNGSLQGLVSWGDPICARPNNRPGYTNLCKTKTWQETIQAN 292

RESULT 9
LIKE HUMAN
```

ID KLKE_HUMAN STANDARD; PRT; 251 AA.
AC Q9P0G3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Kallikrein 14 precursor (EC 3.4.21.-) (Kallikrein-like protein 6) (KIK-16).
GN KLIK14 OR KLIK16.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yousef G.M., Diamandis E.P.;
RT "Molecular characterization, mapping, and tissue expression of KLIK16, a hormonally regulated kallikrein-like gene."
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RA Hooper J.D., Bul L.T., Rae F.K., Harvey T.J., Myers S.A., Ashworth L.K., Clements J.A.;
RT "Identification and characterization of KLIK14, a novel kallikrein serine protease gene located on human chromosome 19q13.4 and expressed in prostate and skeletal muscle."
RL Genomics 73:117-122(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V., Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S., Phan H., Velasco N., Do L.T., Regala W., Terry A., Brower A., Barnes J., Dangnan L., Eiler A., Christensen M., Georgescu A., Avila J., Liu S., Andeise T., Trankheim M., Atlix C., Amico-Keller G., Coesfield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.S., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;
RT "Sequence analysis of chromosome 19q13.4."
RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
RN [4]
RP TISSUE SPECIFICITY.
RA MEDLINE=20545474; PubMed=10969073;
RA Harvey T.J., Hooper J.D., Myers S.A., Stephenson S.A., Ashworth L.K., Clements J.A.;
RT "Tissue-specific expression patterns and fine mapping of the human Kallikrein (KIK) locus on proximal 19q13.4."
RL J. Biol. Chem. 275:37397-37406(2000).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN, BONE MARROW AND FETAL LIVER. ALSO EXPRESSED IN LIVER, PANCREAS, PETAL SPLEEN, PROSTATE AND SKELETAL MUSCLE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC -----
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CC -----
DR EMBL: AF161221; AAD50773.2; -
DR EMBL: AF283669; AAK48523.1; -
DR EMBL: AF283670; AAK48524.1; -
DR EMBL: AC011473; AAG3260.1; -
DR HSSP: P00763; IDPO.
DR MEROPS: S01.029; -
DR Genew: HGNC:6362; KLIK14.
DR MIM: 606135; -
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin.1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; Tryp_Spec; 1.

DR PROSITE: PSS0240; TRYPSIN_DOM; 1.
DR PROSITE: PSS00134; TRYPSIN_HIS; 1.
DR PROSITE: PSS00135; TRYPSIN_SER; 1.
KW Hydroxylase, Serine protease, Signal, Zymogen.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 251
FT ACT_SITE 67 67
FT ACT_SITE 111 111
FT ACT_SITE 204 204
FT DISULFID 31 164
FT DISULFID 52 68
FT DISULFID 143 210
FT DISULFID 175 189
FT DISULFID 200 225
SO SEQUENCE 251 AA; 27452 MW; 9087953BAFA7D25 CRC64;
Query Match 49.3%; Score 623; DB 1; Length 251;
Best Local Similarity 48.9%; Pred. No. 3.9e-50;
Matches 113; Conservative 38; Mismatches 74; Indels 6; Gaps 2;
QY 1 RIIFGECRPHSOPMOALF--EKTRLCGATLIAPRWLTFAHCLKPRYIHLGQHNQ 58
DB 24 KIIGGHTCTRSSQPMQALLACPRRFLCGALISQGVITTAHCGRPILQVALGKHNR 83
QY 59 KEKGCEQTRPATESPPHGFENNSLPKNDHNDIMLVKMASPVSTWAVRPLTSSRCVTA 118
DB 84 RWEATQVLRVRYQVTHPNVN----SRTHNDMLLQGPARGRAVPIETVQACASP 139
QY 119 GTSCLISGSGTSRSPQLRPLRLKCANITIEKQCEKNAIPGNTIDWVCASVQEGKDS 178
DB 140 GTSICRSVGGTISLSPARPAALCVNINISPEVCQKYPRTIIPGMVACAGVPGKDS 199
QY 179 CGDSGSGPLVNCQSLGIGSGODPCAIRKPGVYTKVCKYDWOETKKN 229
DB 200 CGDSGSGPLVNCQSLGIGSGODPCAIRKPGVYTKVCKYDWOETKKN 250
RESULT 10
ID KLIK_RAT STANDARD; PRT; 261 AA.
AC P00758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glandular kallikrein, pancreatic 1 precursor (EC 3.4.21.35) (Tissue kallikrein) (PS kallikrein) (RKG-1).
GN KLIK OR KLIK-1.
OS Rattus norvegicus (rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=83117659; PubMed=6961406;
RA Swift G.H., Dagorn J.-C., Ashley P.L., Cummings S.W., McDonald R.J.;
RT "Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid sequence of the encoded preproenzyme."
RL Proc. Natl. Acad. Sci. U.S.A. 79:7263-7267(1982).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Submaxillary gland;
RC MEDLINE=86051477; PubMed=2998455;
RA Ashley P.L., MacDonald R.J.;
RT "Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of four distinct types including tonin."
RL Biochemistry 24:4512-4520(1985).
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE=Kidney;
RC MEDLINE=89327211; PubMed=2753879;
RA Inoue H., Fukui K., Miyake Y.;
RT "Identification and structure of the rat true tissue kallikrein gene

RT expressed in the kidney."
 RL J. Biochem. 105:834-840(1989).
 RN (14)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89214217; PubMed=2708383;
 RA Mines D.R., Brady J.M., Pritchett D.B., Roberts J.L., Macdonald R.J.;
 RT "Organization and expression of the rat kallikrein gene family."
 RL J. Biol. Chem. 264:7653-7662(1989).
 RN (5)
 RP SEQUENCE OF 48-261 FROM N.A.
 RX MEDLINE=86131678; PubMed=3004582;
 RA Gerald W.L., Chao J., Chao L.;
 RT "Immunological identification of rat tissue kallikrein cDNA and
 characterization of the kallikrein gene family."
 RL Biochim. Biophys. Acta 866:1-14(1986).
 CC -1- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS
 CC IN KININOGEN TO RELEASE LYS-BRADYKININ.
 CC -1- CATALYTIC ACTIVITY: preferential cleavage of Arg-|-Xaa bonds in
 CC small molecule substrates. Highly selective action to release
 CC kallidin (lysyl-bradykinin) from kininogen involves hydrolysis of
 CC Met-|-Xaa or Leu-|-Xaa.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J00758; ; NOT_ANNOTATED_CDS.
 DR EMBL: M11563; AAA41464.1; ALT_INIT.
 DR EMBL: M23876; AAA41462.1; -.
 DR EMBL: M23874; AAA41462.1; JOINED.
 DR EMBL: M23875; AAA41462.1; JOINED.
 DR EMBL: D00448; BAA00346.1; ALT_INIT.
 DR EMBL: D00446; BAA00346.1; JOINED.
 DR EMBL: D00447; BAA00346.1; JOINED.
 DR EMBL: X03560; CAA27247.1; -.
 DR PIR: A00944; KORTP.
 DR PIR: A23863; A23863.
 DR PIR: JX0073; JX0073.
 DR PIR: A33359; A33359.
 DR HSSP: P00757; ISGF.
 DR MEROPS: S01.405; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser.protease_Try.
 DR Pfam: PF00089; trypsin.1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP_SPC.1.
 DR PROSITE: PS50240; TRYPsin.DOM.1.
 DR PROSITE: PS00134; TRYPsin.HIS.1.
 DR PROSITE: PS00135; TRYPsin_SER.1.
 KW Hydrolase; serine protease; Glycoprotein; Multigene family; Zymogen;
 KW Signal.
 FT SIGNAL 1 18
 FT PROPEP 1 24 PROBABLE.
 FT CHAIN 25 261 ACTIVATION PEPTIDE (PROBABLE).
 FT CHAIN 25 261 GLANDULAR KALLIKREIN 1.
 FT CHAIN 111
 FT CHAIN 112 261 CHAIN 2.
 FT ACT_SITE 65 65 CHARGE RELAY SYSTEM.
 FT ACT_SITE 120 120 CHARGE RELAY SYSTEM.
 FT ACT_SITE 213 213 CHARGE RELAY SYSTEM.
 FT DISULFID 31 173 BY SIMILARITY.
 FT DISULFID 50 66 BY SIMILARITY.
 FT DISULFID 152 219 BY SIMILARITY.
 FT DISULFID 184 198 BY SIMILARITY.
 FT DISULFID 209 234 BY SIMILARITY.
 FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (PROBABLE).
 SQ SEQUENCE 261 AA; 28852 MW; F2F99C0227A7882B CRC64;
 Query Match 48.3%; Score 610.5; DB 1; Length 261;

Best Local Similarity 45.6%; Pred. No. 5.7e-49;
 Matches 108; Conservative 43; Mismatches 79; Indels 7; Gaps 1;
 QY 1 RIIFGECKPSPQWQALFEKTRILGATLIAPRWLITAAHCKPRTYVHGOHNILOKE 60
 Db 24 RVAGGYNENMSQPMQVAVYFEGELCGVILDSWVITAAHCATDNQVWLGRRNLVED 83
 QY 61 EGCEQRTATESPPHPGFNNLSL-----PKKHNDIMLVKMSPSVITAAVRLTSS 113
 Db 84 EPFAQHRVLSQSPFHPGFNNLSL-----PKKHNDIMLVKMSPSVITAAVRLTSS 113
 QY 114 RCYVAGTSCILSGWSTSSPOLRLPHLRCAHNTIIEHCKENAVPGNITPTWCASVQE 173
 Db 144 EEPVAGTSCILSGWSTSSPOLRLPHLRCAHNTIIEHCKENAVPGNITPTWCASVQE 203
 QY 174 GKRSCGDSGSPYVQNSLOGISGODPCATRRKPGVYKCKYVDIOTKKNN 230
 Db 204 GKRSCGDSGSPYVQNSLOGISGODPCATRRKPGVYKCKYVDIOTKKNN 260
 RESULT 11
 KLLC_HUMAN STANDARD; PRT; 248 AA.
 AC 09UKR0; 09UKR1; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5)
 DE (KLLC-15)
 GN KLLC12 OR KLLC15.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20118156; PubMed=10652563;
 RA Youset G.M., Luo L.-Y., Diamandis E.P.;
 RT "Identification of novel human kallikrein-like genes on chromosome
 RT 19q13.3-q13.4."
 RL Anticancer Res. 19:2843-2852(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RA Youset G.M., Magklara A., Scorillas A., Diamandis E.P.;
 RT "Cloning of new alternatively spliced forms of the kallikrein-like
 RT gene 5 (KLLC-15)."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20510030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuall J.,
 RA Moss P., Paepel B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region."
 RL Gene 257:119-130(2000).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Iamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez W., Stillaegen S.,
 RA Phan H., Velasco N., Do U., Regala W., Terry A., Brower A., Ganes J.,
 RA Danganan L., Ertler A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andreise T., Frankel M., Altix C., Amico-Keller G., Coeffield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carraro A.V.;
 RT "Sequence analysis of chromosome 19q13.4."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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QY 1 RIIFGECKPHSQPWAALFEKTRLLCGATLIARWLLTAHCKPRYIYHGOHLOKE 60
 DB 24 RIVIGFCEKNSQPMOAWLFTFYKLGVLIDPSWVITTAHCSNNQYWLGNLLEED 83
 QY 61 EGCQOTRATESPFPHPGNNLSL-----PKDHRNDIMLVKMASPVSYMAVPRLLSS 113
 DB 84 EPPAQHPLVSGSEPHPYKPRFLMRNHRKREDDHSDMLMLHLSQPADIDTGVVIDLPT 143
 QY 114 RCYVAGTSCILSGWSTSSPOLRLPHLRCAANTIIEHOKCENAYPCNITDVTWCASVOE 173
 DB 144 EEPVAGSTCLASGWSGTRKPLMERFPDLOQCNHILSNCKIKRYKRYVDMLACAGELE 203
 QY 174 GKDSCGDSGGPLVNCQSLQGIISWGODPCATIRKPGVYTKVCKYVDWIQETMKN 230
 DB 204 GKDTCTGDSGGLCDGVLOGITSMGSCVCAKTNMPATYTKLKFTSMWKEVAKEN 260
 RESULT 13
 KLR3_MOUSE STANDARD; PRT; 261 AA.
 ID KLR3_MOUSE
 AC P00756;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Glandular kallikrein K3 precursor (EC 3.4.21.35) (Tissue kallikrein)
 DE (mGK-3) (7S nerve growth factor gamma chain) (Gamma-NGF).
 GN KLR3 OR KLR-3 OR NGFG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85076169; PubMed=6548955;
 RA Ullrich A., Gray A., Wood W.I., Hayflick J., Seeburg P.H.;
 RT "Isolation of a cDNA clone coding for the gamma-subunit of mouse
 RT nerve growth factor using a high-stringency selection procedure.";
 RL DNA 3:387-392(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85257431; PubMed=3848399;
 RA Evans B.A., Richards R.I.;
 RT "Genes for the alpha and gamma subunits of mouse nerve growth factor
 RT are contiguous.";
 RL EMBO J. 4:133-138(1985).
 RN [3]
 RP SEQUENCE OF 25-261.
 RX MEDLINE=81264363; PubMed=7263706;
 RA Thomas K.A., Beglan N.C., Bradshaw R.A.;
 RT "The amino acid sequence of the gamma-subunit of mouse submaxillary
 RT gland 7 S nerve growth factor.";
 RL J. Biol. Chem. 256:9156-9166(1981).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (3.15 ANGSTROMS) OF 7S COMPLEX.
 RC STRAIN=Swiss Webster; TISSUE=Submaxillary gland;
 RX MEDLINE=8035451; PubMed=9351801;
 RA Bax B., Blundell T.L., Murray-Rust J., McDonald N.O.;
 RT "Structure of mouse 7S NGF: a complex of nerve growth factor with
 RT four binding proteins.";
 RL Structure 5:1275-1285(1997).
 CC -1- FUNCTION: 7S NGF ALPHA CHAIN STABILIZES THE 7S COMPLEX. THE BETA
 CC DIMER PROMOTES NEURITE GROWTH. THE GAMMA CHAIN IS AN ANGININE-
 CC SPECIFIC PROTEASE; IT MAY ALSO HAVE PLASMINOGEN ACTIVATOR
 CC ACTIVITY, AS WELL AS MITOGENIC ACTIVITY FOR CHICK EMBRYO
 CC FIBROBLASTS.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-I-Xaa bonds in
 CC small molecule substrates. Highly selective action to release
 CC kallidin (Lysyl-Diarginine) from kininogen involves hydrolysis of
 CC Met-I-Xaa or Leu-I-Xaa.
 CC -1- SUBUNIT: 7S NERVE GROWTH FACTOR IS COMPOSED OF TWO ALPHA CHAINS,
 CC A BETA DIMER COMPOSED OF IDENTICAL CHAINS, AND TWO GAMMA CHAINS.
 CC -1- MISCELLANEOUS: THIS PRECURSOR IS CLEAVED INTO SEGMENTS TO PRODUCE
 CC THE ACTIVE FORM OF THE GAMMA CHAIN, WHICH OCCURS NATURALLY AS

CC COMBINATIONS OF EITHER TWO OR THREE SEGMENTS HELD TOGETHER BY
 CC DISULFIDE BONDS: B1 + A OR B1 + C + B2.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X01389; CAA25645.1; -
 CC EMBL: X01798; CAA25928.1; -
 CC EMBL: X01799; CAA25930.1; -
 CC PIR: A00942; NCMSG.
 CC PDB: 1SGF; 27-MAY-98.
 CC MEROPS: S01.170; -.
 CC MGD: MGI:97322; Ngfg.
 CC Interpro: IPR001314; Chymotrypsin.
 CC Interpro: IPR001254; Ser_protease_Try.
 CC Pfam: PF00089; trypsin; 1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC SMART: SM00020; TRYPSIN_DOM; 1.
 CC PROSITE: PS50240; TRYPSIN_DOM; 1.
 CC PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC PROSITE: PS00135; TRYPSIN_SER; 1.
 CC KMW Hydrolyase: Serine protease; Glycoprotein; Multigene family; Zymogen;
 CC Signal; Growth factor; 3D-structure.
 CC FT SIGNAL 1 18 PROBABLE.
 CC FT PROPEP 19 24 ACTIVATION PEPTIDE.
 CC FT CHAIN 25 261 GLANDULAR KALLIKREIN K3.
 CC FT CHAIN 25 107 NERVE GROWTH FACTOR GAMMA CHAIN 1.
 CC FT CHAIN 112 261 NERVE GROWTH FACTOR GAMMA CHAIN 2.
 CC FT ACT_SITE 65 65 CHARGE RELAY SYSTEM.
 CC FT ACT_SITE 120 120 CHARGE RELAY SYSTEM.
 CC FT ACT_SITE 213 213 CHARGE RELAY SYSTEM.
 CC FT DISULFID 31 173
 CC FT DISULFID 50 66
 CC FT DISULFID 152 219
 CC FT DISULFID 184 198
 CC FT DISULFID 209 234
 CC FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .).
 CC FT DOMAIN 25 107 SEGMENT B1.
 CC FT DOMAIN 112 261 SEGMENT A.
 CC FT DOMAIN 112 164 SEGMENT C.
 CC FT DOMAIN 165 261 SEGMENT B2.
 CC FT CONFLICT 108 111 MISSING (IN REF. 2).
 CC SQ SEQUENCE 261 AA; 28998 MW; 4870748E174AF7C8 CRC64;
 CC -----
 CC Query Match 47.5%; Score 600.5; DB 1; Length 261;
 CC Best local Similarity 44.7%; Pred. No. 4.7e-48;
 CC Matches 106; Conservative 46; Mismatches 78; Indels 7; Gaps 1;
 CC -----
 CC QY 1 RIIFGECKPHSQPWAALFEKTRLLCGATLIARWLLTAHCKPRYIYHGOHLOKE 60
 DB 24 RIVIGFCEKNSQPMOAWLFTFYKLGVLIDPSWVITTAHCSNNQYWLGNLLEED 83
 QY 61 EGCQOTRATESPFPHPGNNLSL-----PKDHRNDIMLVKMASPVSYMAVPRLLSS 113
 DB 84 EPPAQHPLVSGSEPHPYKPRFLMRNHRKREDDHSDMLMLHLSQPADIDTGVVIDLPT 143
 QY 114 RCYVAGTSCILSGWSTSSPOLRLPHLRCAANTIIEHOKCENAYPCNITDVTWCASVOE 173
 DB 144 EEPVAGSTCLASGWSGTRKPLMERFPDLOQCNHILSNCKIKRYKRYVDMLACAGEMD 203
 QY 174 GKDSCGDSGGPLVNCQSLQGIISWGODPCATIRKPGVYTKVCKYVDWIQETMKN 230
 DB 204 GKDTCTGDSGGLCDGVLOGITSMGSCVCAKTNMPATYTKLKFTSMWIKIYMAKN 260
 RESULT 14
 KLR3_PRANA

ID KLRK_PRANA STANDARD; PRT; 263 AA.
AC P32824;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Glandular kallikrein, renal precursor (EC 3.4.21.35) (Tissue kallikrein).
OS Prionys natalensis (African soft-furred rat) (Mastomys natalensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mastomys.
OX NCBI_TaxID=10112;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RX MEDLINE=94226702; PubMed=7909667;
RA Farnesstock M.;
RT "Characterization of kallikrein cDNAs from the African rodent Mastomys".
RL DNA Cell Biol. 13:293-300(1994).
CC -1- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS IN KININOGEN TO RELEASE LYS-BRADYKININ.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-I-Xaa bonds in small molecule substrates. Highly selective action to release kallidin (lysyl bradykinin) from kininogen involves hydrolysis of Met-I-Xaa or Leu-I-Xaa.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC -----
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CC -----
DR EMBL: X17352; CA35232.1; -
DR PIR: S15686; S15686.
DR HSP: P00757; 1SGF.
DR MEROPS: S01.160; -
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PRO0722; CHYMOTRYPSIN.
DR SMART: SM00020; tryp-Spc; 1.
DR PROSITE: PS50240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KM Hydrolyse; Serine protease; Glycoprotein; Multigene family; zymogen;
KW Signal.
FT SIGNAL 1 18 PROBABLE.
FT PROPEP 19 24 ACTIVATION PEPTIDE (PROBABLE).
FT CHAIN 25 263 GLANDULAR KALLIKREIN, RENAL.
FT ACT_SITE 65 65 CHARGE RELAY SYSTEM.
FT ACT_SITE 121 121 CHARGE RELAY SYSTEM.
FT ACT_SITE 215 215 CHARGE RELAY SYSTEM.
FT DISULFID 31 175 BY SIMILARITY.
FT DISULFID 50 66 BY SIMILARITY.
FT DISULFID 153 221 BY SIMILARITY.
FT DISULFID 186 200 BY SIMILARITY.
FT DISULFID 211 236 BY SIMILARITY.
FT CAROHND 102 102 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 263 AA; 29130 MM; A8EB023B800337D5 CRC64;
Query Match 47.2%; Score 596.5; DB 1; Length 263;
Best Local Similarity 44.8%; Pred. No. 1,le-47;
Matches 107; Conservative 44; Mismatches 79; Indels 9; Gaps 2;
QY 1 RIHKGEKPHSQPQALFEKTRLLCATLAPRLTLTAACLPKRYVHGOHLQRE 60
DB 24 RIIGFENCENKSNQPMHVAVYRFRAGCGVLLDAMWVLAALCAICNDKYVWLGKNNRFED 83
OY 61 ECGEOTRTATESFPHGPNFNSLPNKRH-----RNDIMLVKMASPVSTWAVRPLTJS 112

DB 84 EPSAQHQLSKALPHDPGFNMSLNKNKDHTRPEDDYSNDLMLVLRKKPAPITFDVVKPIDLP 143
OY 113 SRCVAGTSCLISGMCSTG-SPQLRLPHTLRCANITIEHOCENYAPGNTIDTVACASY 171
DB 144 TEEPTVGSRCISAGSGSTTPTEFEYSHDLCYVLELLNEVCARAKHTKVDITMLCAGE 203
OY 172 OEGKDSOCODSGCPVLCNOSLOGITISMGODPCATRRKGVYTKVCKVYVDIOETMKN 230
DB 204 MDGKDTGVGDSGGLICDVGLOGITISMGPTPCALPNVGIYTKLEYSRWIKDVANN 262
RESULT 15
TRY3_CHICK
ID TRY3_CHICK STANDARD; PRT; 248 AA.
AC Q90629;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Trypsin II-p29 precursor (EC 3.4.21.4).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=pancreas;
RX MEDLINE=95251611; PubMed=7733885;
RA Wang K., Gan L., Lee I., Hood L.E.;
RT Isolation and characterization of the chicken trypsinogen gene family.";
RL Biochem. J. 307:471-479(1995).
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-I-Xaa, Lys-I-Xaa.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: HIGH LEVELS ARE SEEN IN THE PANCREAS WHILE LOWER LEVELS ARE FOUND IN THE LIVER, SPLEEN AND THYMUS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -----
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CC -----
DR EMBL: U15157; AAA79914.1; -
DR HSP: P00763; IDPO.
DR MEROPS: S01.151; -
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PRO0722; CHYMOTRYPSIN.
DR SMART: SM00020; tryp-Spc; 1.
DR PROSITE: PS50240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KM Hydrolyse; Serine protease; Digestion; Pancreas; zymogen; Signal;
KW Multigene family.
FT SIGNAL 1 16 BY SIMILARITY.
FT PROPEP 17 25 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 26 248 TRYPSIN II-p29.
FT ACT_SITE 65 65 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 109 109 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 202 202 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 32 162 BY SIMILARITY.
FT DISULFID 50 66 BY SIMILARITY.
FT DISULFID 134 235 BY SIMILARITY.
FT DISULFID 141 208 BY SIMILARITY.
FT DISULFID 173 187 BY SIMILARITY.
FT DISULFID 196 222 BY SIMILARITY.
FT SITE 196 196 REQUIRED FOR SPECIFICITY (BY SIMILARITY).

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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 23, 2002, 14:23:37 ; Search time 69 Seconds
(without alignments)
1022.256 Million cell updates/sec

Title: US-09-856-320A-2_COPY_53_282

Perfect score: 1263

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Ygapop 10.0	Ygapext 0.5	
Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-blosum62 -TRANS-human40.csl
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-WARN_TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents.NA.*
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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1263	100.0	1192	4	US-08-944-483-8
2	1263	100.0	1314	3	US-09-025-059-2
3	1251	99.0	1166	4	US-08-944-483-7
4	1221.5	96.7	1052	4	US-09-386-642-10
5	1218	96.4	833	2	US-08-790-137-2
6	916.5	72.6	618	4	US-09-280-116-3
7	683	54.1	944	3	US-09-070-526-1
8	675	53.4	994	4	US-09-008-271A-19
9	673.5	53.3	1049	4	US-09-386-642-9
10	636.5	50.4	1476	2	US-08-824-874-2
11	636.5	50.4	1476	4	US-09-210-084-2
12	634.5	50.2	1364	4	US-09-280-116-20

13	582.5	46.1	766	3	US-08-768-859A-9	Sequence 9, Appl1
14	582.5	46.1	766	3 <td>US-08-767-820A-9</td> <td>Sequence 9, Appl1</td>	US-08-767-820A-9	Sequence 9, Appl1
15	582.5	46.1	766	3 <td>US-08-622-046B-17</td> <td>Sequence 17, Appl1</td>	US-08-622-046B-17	Sequence 17, Appl1
16	582.5	46.1	766	4 <td>US-09-100-264-6</td> <td>Sequence 6, Appl1</td>	US-09-100-264-6	Sequence 6, Appl1
17	582.5	46.1	822	4 <td>US-09-100-264-8</td> <td>Sequence 8, Appl1</td>	US-09-100-264-8	Sequence 8, Appl1
18	582.5	46.1	832	3 <td>US-08-768-859A-5</td> <td>Sequence 5, Appl1</td>	US-08-768-859A-5	Sequence 5, Appl1
19	582.5	46.1	832	3 <td>US-08-767-820A-5</td> <td>Sequence 5, Appl1</td>	US-08-767-820A-5	Sequence 5, Appl1
20	582.5	46.1	832	3 <td>US-08-622-046B-15</td> <td>Sequence 15, Appl1</td>	US-08-622-046B-15	Sequence 15, Appl1
21	582.5	46.1	1341	4 <td>US-08-983-075D-6</td> <td>Sequence 6, Appl1</td>	US-08-983-075D-6	Sequence 6, Appl1
22	582.5	46.1	1358	4 <td>US-08-983-075D-8</td> <td>Sequence 8, Appl1</td>	US-08-983-075D-8	Sequence 8, Appl1
23	579.5	45.9	766	3 <td>US-08-622-046B-6</td> <td>Sequence 6, Appl1</td>	US-08-622-046B-6	Sequence 6, Appl1
24	579.5	45.9	832	3 <td>US-08-768-859A-20</td> <td>Sequence 20, Appl1</td>	US-08-768-859A-20	Sequence 20, Appl1
25	579.5	45.9	832	3 <td>US-08-767-820A-20</td> <td>Sequence 20, Appl1</td>	US-08-767-820A-20	Sequence 20, Appl1
26	579.5	45.9	832	3 <td>US-08-622-046B-4</td> <td>Sequence 4, Appl1</td>	US-08-622-046B-4	Sequence 4, Appl1
27	579	45.8	732	1 <td>US-08-361-395-2</td> <td>Sequence 2, Appl1</td>	US-08-361-395-2	Sequence 2, Appl1
28	579	45.8	897	2 <td>US-08-956-267A-1</td> <td>Sequence 1, Appl1</td>	US-08-956-267A-1	Sequence 1, Appl1
29	578.5	45.8	766	5 <td>PCT-US95-06157-9</td> <td>Sequence 9, Appl1</td>	PCT-US95-06157-9	Sequence 9, Appl1
30	578.5	45.8	832	5 <td>PCT-US95-06157-5</td> <td>Sequence 5, Appl1</td>	PCT-US95-06157-5	Sequence 5, Appl1
31	577.5	45.7	711	3 <td>US-08-622-046B-13</td> <td>Sequence 13, Appl1</td>	US-08-622-046B-13	Sequence 13, Appl1
32	577.5	45.7	711	4 <td>US-09-100-264-2</td> <td>Sequence 2, Appl1</td>	US-09-100-264-2	Sequence 2, Appl1
33	577.5	45.7	760	3 <td>US-08-768-859A-7</td> <td>Sequence 7, Appl1</td>	US-08-768-859A-7	Sequence 7, Appl1
34	577.5	45.7	760	3 <td>US-08-767-820A-7</td> <td>Sequence 7, Appl1</td>	US-08-767-820A-7	Sequence 7, Appl1
35	575	45.5	1504	4 <td>US-09-280-116-1</td> <td>Sequence 1, Appl1</td>	US-09-280-116-1	Sequence 1, Appl1
36	574.5	45.5	711	3 <td>US-08-622-046B-2</td> <td>Sequence 2, Appl1</td>	US-08-622-046B-2	Sequence 2, Appl1
37	573.5	45.4	760	5 <td>PCT-US95-06157-7</td> <td>Sequence 7, Appl1</td>	PCT-US95-06157-7	Sequence 7, Appl1
38	566	44.8	825	3 <td>US-09-120-82-1</td> <td>Sequence 1, Appl1</td>	US-09-120-82-1	Sequence 1, Appl1
39	556.5	44.1	992	1 <td>US-08-358-782D-13</td> <td>Sequence 13, Appl1</td>	US-08-358-782D-13	Sequence 13, Appl1
40	556.5	44.1	992	2 <td>US-08-764-527A-13</td> <td>Sequence 13, Appl1</td>	US-08-764-527A-13	Sequence 13, Appl1
41	556.5	44.1	1462	2 <td>US-08-358-782D-14</td> <td>Sequence 14, Appl1</td>	US-08-358-782D-14	Sequence 14, Appl1
42	556.5	44.1	1462	2 <td>US-08-764-527A-14</td> <td>Sequence 14, Appl1</td>	US-08-764-527A-14	Sequence 14, Appl1
43	551.5	43.7	711	4 <td>US-09-100-264-4</td> <td>Sequence 4, Appl1</td>	US-09-100-264-4	Sequence 4, Appl1
44	549.5	43.5	1729	4 <td>US-08-844-024-1</td> <td>Sequence 1, Appl1</td>	US-08-844-024-1	Sequence 1, Appl1
45	549.5	43.5	1729	2 <td>US-08-718-547-1</td> <td>Sequence 1, Appl1</td>	US-08-718-547-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-944-483-8
; Sequence 8, Application US/08944483
; Patent No. 6232456

GENERAL INFORMATION: 2061

APPLICANT: COHEN, MAURICE
APPLICANT: COLETTIS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANAPOS, EDWARD N.
APPLICANT: KLISS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944, 483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1192 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-856-320A-2
US-09-856-320A-2_COPY_53_282 (1-230) x US-08-944-483-8 (1-1192)
Alignment Scores:
Pred. No.: 3.08e-124 Length: 1192
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 4
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QY 1 ArgTLeIleIleYsglyPheglucYslyProHISerGlnProTyrGlnAlaAlaLeuPhe 20
DB 167 AGGATCATCAAGGGGCTCGAGTGCAGACCCCTACATCCAGCCCTGGGAGGAGCCCTGTC 226
QY 21 GlulysThrArgLeuLeuYsglyAlaThrLeuLeaLProArgTyrLeuLeuThrAla 40
DB 227 GAGAAAGACGGGGCTACTCTGTGGGGCAGCCTATCCGCCAGATGGCTCTGACAGCA 286
QY 41 AlaHIScYsLeuYsProArgTyrIleValHISleuGlyGlnHISAsnLeuGlnIlysglu 60
DB 287 GCCCAGCTGCTCAAGCCCTCTACATAGTTCACCTGGGGGAGGACCAACCTCCAGAAAGAG 346
QY 61 GlulGlyCysgluGlnThrArgThrAlaThrGluSerPheProHISProGlyPheAsnAsn 80
DB 347 GAGGGGCTGTAGCAGACCCGAGACGACCTGAGTCTCCGCCACCCGGGCTTCAACAC 406
QY 81 SerLeuProAsnIlySAspHISArgAsnAspIleMetLeuValIlySmetAlaSerProVal 100
DB 407 AGCCTCCCAACAAAGCCACCCCAATGACATATGCTGTGAAGATGGCATCGCCAGTC 466
QY 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
DB 467 TCCATCACCTGGGCTGTGGCAGCCCTCACCTCTCTCACGCTGTGTCTGCTGCGCACC 526
QY 121 SerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHISThr 140
DB 527 AGCGGCTCATTTCCGGCTGGGGAGAGACGTCCAGCCCCAGTTAGCGCTTCACAC 586
QY 141 LeuArgCysAlaAsnIleThrIleGlnHISGlnIlySglnAsnAlaTyrProGly 160
DB 587 TTGCGATGCCCAACATCACATCATTTGACACAGAAAGTGTGAAGACGCTACCCCGG 646
QY 161 AsnIleThrAspHISMetValCysAlaSerValGlnGlnIlyGlyIlySAspSerCysGln 180
DB 647 AACATCACACACACACAGGTGTGTGCCAGGTCCAGAAAGGGGCAAGGACCTCTCCAG 706
QY 181 GlyAspSerGlyIlyProLeuValCysAsnGlnSerLeuGlnIlyIleIleSerTPGly 200
DB 707 GGTGATCTCGGGGGCCCTCTGTGTCTGTAAACACTCTTCAAGCATATATCTCTGGGG 766
QY 201 GlnAspProCysAlaIleThrArgIlyProGlyValIlyThrIlySValCysIlyTyrVal 220
DB 767 CAGGATCCGTTGCGATTCACCCGAAAGCCGTGTCTACACGAAAGTGTGCAAAATATGTG 826
QY 221 AspTyrIleGlnIlyThrArgThrAlaThrGluSerPheProHISProGlyPheAsnAsn 230
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DB 827 GACTGATCCAGACGATGAAGACAAAT 856
RESULT 2
US-09-025-059-2
Sequence 2, Application us/09025059
Patent No. 6075136
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guebler, Neil J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,059
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0481 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNG T10
CLONE: 2723646
US-09-025-059-2
US-09-856-320A-2_COPY_53_282 (1-230) x US-09-025-059-2 (1-1314)
Alignment Scores:
Pred. No.: 3.57e-124 Length: 1314
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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DB 284 AGGATCATCAAGGGGCTTCAGATGCAAGCTCTACCTCCAGCCCTGGGAGGAGCCCTGTTG 343
QY 21 GlulysThrArgLeuLeuYsglyAlaThrLeuLeaLProArgTyrLeuLeuThrAla 40
DB 344 GAGAAAGCAGGCTACTCTGTGGGGGAGGAGCTATCGCCCAAGATGCTCTGACAGCA 403
QY 41 AlaHIScYsLeuYsProArgTyrIleValHISleuGlyGlnHISAsnLeuGlnIlysglu 60
DB 404 GCCCAGCTGCTCAAGCCCTCTACATAGTTCACCTGGGGGAGGACCAACCTCCAGAAAGAG 463
QY 61 GlulGlyCysgluGlnThrArgThrAlaThrGluSerPheProHISProGlyPheAsnAsn 80
|||||

|||||
Db 464 GAGGGCTGTGACACACCCGGACACCACTAGTCTTCCGCCACCCGGCTTCAACAC 523
Qy 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
Db 524 AGCTCCCAACAAAGACACCGCATCATCATGCTGGTGGMAATGGATCGCCAGTC 583
Qy 101 SerIleThrPAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
Db 584 TCCATCACCCTGGGCTGTGCGAACCCCTCCCTCCACCGCTGTGTCACGCTGGGACC 643
Qy 121 SerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
Db 644 AGCTGCCCTATTTCGGCTGGGGACGACGTCAGCCGCCAGTTACGCTCCACACAC 703
Qy 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGly 160
Db 704 TTGCATCGCCCAACATCATCATCATTTAGACACCAAGATGTGMAAGCCTTACCCGGC 763
Qy 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
Db 764 AACATCAGACAGACCATGCTGTGTCCAGCTGCAGAGAGGGGCAAGACTCCCTGCAG 823
Qy 181 GlyAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGly 200
Db 824 GGTGACTCCGGGGGCCCTGTGCTGTACCAAGTCTTCAAGGCATTATCTCTGGGGC 883
Qy 201 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 220
Db 884 CAGATCGCTGTGCGATACCCCGAAGCCTGTGTCTTACAGAAAGTCTGCAATATGTG 943
Qy 221 AspTyrIleGlnIleThrMetLysAsnAsn 230
Db 944 GACTGATCCAGAGACGATGAAGAACAT 973

RESULT 3
US-08-944-483-7
; Sequence 7, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLETTIS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLAS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.

2001

REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183 US .01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1166 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-944-483-7

Alignment Scores:
Pred. No.: 5,53e-123 Length: 1166
Score: 1251.00 Matches: 228
Percent Similarity: 99.13% Conservative: 0
Best Local Similarity: 99.13% Mismatches: 2
Query Match: 99.05% Indels: 0
DB: Caps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x US-08-944-483-7 (1-1166)

Qy 1 ArgIleIleLysGlyPheGluCysLysProHisSerGlnProTyrGlnAlaAlaLeuPhe 20
Db 163 AGGATCATCAAGGGGTTGAGTGCAGTCAGCCATCCAGCCCTGGAGGAGCCCTGTGC 222
Qy 21 GluLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTyrPheLeuThrAla 40
Db 223 RAGAAACGGCGGTACTCTGTGGGGCGAGCTATCGCCCCCAATGATGCTCTGCACAGCA 282
Qy 41 AlaHisCysLeuLysProArgTyrIleValHisLeuGlnHisAsnLeuGlnLysGlu 60
Db 283 GCCCACTGCCCTCAAGCCCGCGTACATAGTTCACCTGGGGCGACCAACCTTCACAAAGAG 342
Qy 61 GluLysCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 80
Db 343 GAGGCGTGTGAGACACCCGGACAGCCAGCTGATCTCCGCCACCCCGGCTTCAACAC 402
Qy 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
Db 403 AGCTCCCAACAAAGACACCGCAATGATCATCTGTGTGGAAGATGGATCGCCAGTC 462
Qy 101 SerIleThrPAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
Db 463 TCCATCACCCTGGGCTGTGCGAACCCCTCACCTCTCTCACCGCTGTGCACCTGGCACC 522
Qy 121 SerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
Db 523 AGTGCTCATTTCCGGCTGGGGCAGCAGCGCCAGCCCGAGTTACGCTGCTCACACC 582
Qy 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGly 160
Db 583 TTGGATCGCCCAACATCATCATCATTTAGACACCAAGATGTGAAAGCGCTTACCCGGC 642
Qy 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
Db 643 AACATCAGACAGACCATGCTGTGTGCCAGCTGCAGAGAGGGGCAAGATCTCTGCAG 702
Qy 181 GlyAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGly 200
Db 703 GGTGACTCCGGGGGCCCTGTGCTGTGTAACCAAGCTCTTCAAGGCATTATCTCTGGGGC 762
Qy 201 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 220
Db 763 CAGGATCGGTGTGCGATCACCCCGAAGCCTGTGTCTTACAGAAAGTCTGCAATATGTG 822
Qy 221 AspTyrIleGlnIleThrMetLysAsnAsn 230
Db 823 GACTGATCCAGAGACGATGAAGAACAT 852

RESULT 4

US-09-386-642-10
; Sequence 10, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Q1, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1052
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-10

210 bp
101-200

Alignment Scores:
Pred. No.: 6, 22e-120 Length: 1052
Score: 1221.50 Matches: 223
Percent Similarity: 98.27% Conservative: 4
Best Local Similarity: 96.54% Mismatches: 3
Query Match: 96.71% Indels: 1
DB: 4 Gaps: 1

US-09-856-320A-2_COPY_53_282 (1-230) x US-09-386-642-10 (1-1052)

QY 1 ArgIleIleLysGlyPheGluCys---LysProHisSerGlnProTrpGlnAlaLeu 19
Db 163 AAGATCGTGGGGCTACACTGCTGAGAAAGACATCCAGCCCTGGGAGGAGCCCTG 222
QY 20 PheGluLysThrArgLeuLeuGlyAlaThrLeuAlaProArgTrpLeuThr 39
Db 223 TTCGAGAAAGAGCGGCTACCTGTGGGCGACCTCATCGCCCGAGATGGCTCTGACA 282
QY 40 AlaAlaHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLys 59
Db 283 GCAGGCCACTGCTCAAGCCCGCTACATGTTCTACCTGGGGAGCAGCACTCCAGAG 342
QY 60 GluGluGlyCysGluGlnThrArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLys 79
Db 343 GAGGAGGGCTGTGAGCAGACCCGAGCAGCAGCTGCTCCCGACCCGCGCTTCAAC 402
QY 80 AsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerPro 99
Db 403 AACAGCCTCCCAACAAAGACACCGCAATGACATCATCTGCTGTAAGATGCGATCGCCA 462
QY 100 ValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGly 119
Db 463 GCTTCATCATCGTGGGCTGTGGACCCCTCACCCTCCCTCAGCGTGTGCTGCTGCG 522
QY 120 ThrSerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHis 139
Db 523 ACCAGCTGCTCATCTTCGCGCTGGGCGAGCAGCTCCAGCCCGAGTTACCTGCTCTCAC 582
QY 140 ThrLeuArgCysAlaAsnIleThrIleGlnHisGlnLysCysGlnAsnAlaIleTrpPro 159
Db 583 ACCCTGCGATGCGCCCAACATCACCATCATTTGACACAGAAAGTGTAGAAAGCGCTTACCC 642
QY 160 GlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCys 179
Db 643 GCGAATCATCAGACACCATGCTGTGTGCGACGCTGCGAGAGAGGGGCAAGGACTCTTGC 702
QY 180 GlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrp 199
Db 703 CAGGCTGACATCCGCGGCGCTGTGCTGTAAACAGACTCTCTTCAAGAGCATTTATCTCTGG 762
QY 200 GlyGlnAspProCysAlaIleThrArgLysProGlyValIleTrpLysValCysLysTrp 219

Db 763 GGCAGAGATCGTGTGAGACACCCGAAAGCCTGCTGTACAGAAAGTCTCAATAT 822
QY 220 ValAspTrpIleGlnGluThrMetLysAsnAsn 230
Db 823 GTGACTGATCCAGAGACGATGAGAACAT 855

RESULT 5

US-08-790-137-2
; Sequence 2, Application US/08790137
; Patent No. 5840871
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goll, Surya K.
; TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED
; TITLE OF INVENTION: KALLIKREIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,137
; FILING DATE: Filed Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0195 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-790-137-2

Alignment Scores:
Pred. No.: 1, 03e-119 Length: 833
Score: 1218.00 Matches: 220
Percent Similarity: 97.83% Conservative: 5
Best Local Similarity: 95.65% Mismatches: 5
Query Match: 96.44% Indels: 0
DB: 2 Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x US-08-790-137-2 (1-833)

QY 1 ArgIleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPhe 20
Db 96 CGATGTGTGGAGCGTGTGAGTGTGAGCAGCATTTCCAGCCCTGGAGCGGCTGTGTC 155
QY 21 GluLysThrArgLeuLeuGlyAlaThrLeuAlaProArgTrpLeuThrAla 40
Db 156 CAGAAAGCGCGCTACTCTGTGGGCGAGGNTCATNGCCCGAGATGTTCTTCAAGCA 215
QY 41 AlaHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
Db 216 GCCCATGCTTNAAGCCCGCTACATATGTTACCTGGGCGAGCAGACACATCCAGAGAG 275

QY 61 GluLysGlySerGluThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsn 80
DB 276 GAGGGCTGTGAGCAGACCCGACAGCCAGTGTCTTCCCGCCAGCCCGGCTTCAACAAAC 335
QY 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
DB 336 AGCTTCCCGCAAGAACACCCGCAATGACATCTGCTGGTGAAGATGGATGCGCCAGTC 395
QY 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
DB 396 TCCATCAACCTGGCTGTGCGACCCCTCACCCCTCTCCACGCTGTGTACATGCTGGAGC 455
QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
DB 456 AGCTGCTCATTTCCGCTGTGGGCGACAGCTCCAGCCCGCATTCACCTGCTCCACACC 515
QY 141 LeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTrpProGly 160
DB 516 TTGGGATGCGCCACATCATCATCATTTGACACAGAAAGTGTGAAGAGGCTTACCCGCG 575
QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnLysGlyLysAspSerCysGln 180
DB 576 AACATCACAGACACCATGT 635
QY 181 GlyAspSerGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 200
DB 636 GGTGACCTCCGCGGCGCTGT 695
QY 201 GluAspProCysAlaIleThrArgLysProGlyValLysThrLysValCysLysTrpVal 220
DB 696 CAGATCATGCTGT 755
QY 221 AspTrpIleGlnLysThrMetLysAsnAsn 230
DB 756 GACTGATCCAGAGACGATGAAGAACAAT 785

P.D. Dec 18, 2001

A-102e

RESULT 6
US-09-280-116-3
; Sequence 3, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-3

Alignment Scores:
Pred. No.: 4, 8e-88 Length: 618
Score: 916.50 Matches: 184
Percent Similarity: 90.788 Conservative: 3
Best Local Similarity: 89.328 Mismatches: 4
Query Match: 72.578 Indels: 16
Gaps: 2

US-09-856-320a-2_copy_53_282 (1-230) x US-09-280-116-3 (1-618)

QY 24 ArgLeuLeuGlyGlyAlaThrLeuIleAlaPro-ArgTrpLeuLeuThrAlaAlaHisCys 43
DB 2 CGCTACTCTGTGTGGGCGAC---TCATCCGCTTCAGATGCTCTGTGACACACCCACTG 58
QY 43 sLeuLysProArgTrpLysValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlyCys 63
DB 59 CCTCAAGCCCGGCTACTAGTCACTGCGGCGACACACCTCCAGAAAGAGAGGCGCTG 118

QY 63 sGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuPr 83
DB 119 TGACAGACCCGAGACAGACACTGATCTCTTCCCGCCAGCCCGGCTTCAACAAACACCTCC 178
QY 83 AsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal-SerIleT 103
DB 179 CACAAAGACCCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 238
QY 103 hTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysL 123
DB 239 CTTGGCTGTGCGACCCCTCACCCCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 298
QY 123 euIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeuArgC 143
DB 299 TCATTTCCGCTGTGGGCGACAGCTCCAGCCCGCATTCACCTGCTCCACACCTTGGAT 358
QY 143 yAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTrpProGlyAsnIleT 163
DB 359 GCGCAACATCACCATCATTTGAGCCACCAAGATGTGAGAACGCTTACCCGCGCAACATCA 418
QY 163 hAspThrMetValCysAlaSerValGlnGlnLysGlyLysAspSerCysGlnLysAsp 183
DB 419 CAGACACCATGT 471
QY 183 ergLysGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrp-GlyGlnAsp 202
DB 472 -----GTCCTTC-AAAGCATTTATCTCTGGGCGCGACAGAC 507
QY 203 -ProCysAlaIleThrArgLysProGlyValTrpThrLysValCysLysTrpValAspTr 222
DB 508 TCCGTGTGATCATCACCCGAAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 567
QY 222 pIleGlnGlu 225
DB 568 GATCCAGGAA 577

P.D. 2000

RESULT 7
US-09-070-526-1
; Sequence 1, Application US/09070526
; Patent No. 6100059
; GENERAL INFORMATION:
; APPLICANT: SOOTHAN, CHRISTOPHER
; APPLICANT: CLINKENBEARD, HELEN
; TITLE OF INVENTION: No. 6100059e1 Compounds
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,526
FILING DATE: 30-APR-1998
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9711952.3
FILING DATE: 9-JUN-1997
APPLICATION NUMBER: EP 9730964.4
FILING DATE: 1-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-30353
TELECOMMUNICATION INFORMATION:

A-102e


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Db 712 CTC-----CACCGTGGCCACTTAACGACCTCATTCATCAAACTGAAACAG 759
Qy 98 rProValserIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAl 118
Db 760 AAGATTGCTCCCACTAAAGATGTCAGACCATCAAGCTCTCTCTCTCTCTCTCTCTGC 819
Qy 118 aGlyThrSerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuPr 138
Db 820 TGGGACAAAGTGTGTGGTCTGGGTCGGGACCAACCAAGAGCCCAAGTGCACCTGCC 879
Qy 138 oHisThrLeuArgCysAlaAsnIleThrIleIleIleIleIleIleIleIleIleIle 158
Db 880 TAAGTCTCTCAAGTCTGTAATTCAGGCTCTAGTCAAGAAAGTCCGAGATGCTTA 939
Qy 158 rProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyIleCysAspSe 178
Db 940 CCCGAGACAGATAGATGACACACATGTTCTGCGCGGT---GACAAAGAGGTAGAGACTC 996
Qy 178 rCysGlnGlyAspSerGlyIleProLeuValCysAsnGlnSerLeuGlnGlyIleIleSe 198
Db 997 CTGCAGAGGTATCTGGGGGCGCTGTGCTGCAATGCTCCCTGCAGGAGTCTGTCTC 1056
Qy 198 rTrpGlyGlnAspProCysAlaIleThrArgIleProGlyValIleThrIleValCysLy 218
Db 1057 CTGGGAGATTATACCTGTGTGCGCGGCCCAACAGACCGGGTGTCAAGCAACTCTGCA 1116
Qy 218 sTyValAspTrpIleGlnGlnIleThrMetIleCysAsnAsn 230
Db 1117 GTTCCACCAAGTGAATCCAGAAACCATCCAGGCCAAC 1153

RESULT 12
US-09-280-116-20/c
: Sequence 20, Application US/09280116A
: Patent No. 6331427
: GENERAL INFORMATION:
: APPLICANT: Robison, Keith E.
: TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
: FILE REFERENCE: 5800-24, 035800/176965
: CURRENT APPLICATION NUMBER: US/09/280,116A
: CURRENT FILING DATE: 1999-03-26
: NUMBER OF SEQ ID NOS: 268
: SOFTWARE: Patent Ver. 2.0
: SEQ ID NO 20
: LENGTH: 1364
: TYPE: DNA
: ORGANISM: Homo sapiens
: OTHER INFORMATION: trypsin-like serine proteases
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(1364)
: OTHER INFORMATION: n = a, t, c, or g
US-09-280-116-20

Alignment Scores:
Pred. No.: 1,01e-57 Length: 1364
Score: 634.50 Matches: 123
Percent Similarity: 64.82% Conservative: 41
Best Local Similarity: 48.62% Mismatches: 60
Query Match: 50.24% Gaps: 29
DB: 4

US-09-856-320A-2_COPY_53_282 (1-230) x US-09-280-116-20 (1-1364)
Qy 5 GlyheGluCysLysProHisSerGlnProTrpGlnAlaIleuPheGlnLysThrArg 24
Db 828 GGGTACACCTGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 769
Qy 25 LeuLeuGlyGlyAlaThr-LeuIleAlaProArgTrpLeuLeuThrAlaIleHisCysLe 44
Db 768 CTACTCTGTGGGGAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 709
Qy 44 uLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlyCysG 64

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Db 708 AAAGAGGGGCTCAAAAGTTTACTAGCAAGCAGCCCTAGGGCGTGTGAAGCTGTGGA 649
Qy 64 uGlnThrArgThrAlaThrGlnUserPheProHisProGlyIleHisAsnSerLeuProAs 84
Db 648 GCAGGTGAGGGAAGTGTGCACCTCTATCCGCCACCTCAAAATCCAGGAGACCCCAACCA 589
Qy 84 nLysAspHisArgAsnAspIleMetLeuValIleSerProValSerIleThrTr 104
Db 588 CCTGACACCAACCATGATCATCTCTCTGAGCTGAGTCCCGGTCCAGCTACAGG 529
Qy 104 pAlaValArgProLeuThrLeuSer---SerArgCysValThrAlaGlyThrSerCysLe 123
Db 528 CTACATCCAAACCTGCGCCCTTCCCAACAAACCGGCTTAACCCCTGACACACCTGTGC 469
Qy 123 uIleSerGlyTrpGlySerThrSerSerProGln-----LeuArg 136
Db 468 GGTGTGTGGTGGGACACACACACACACACACACACACACACACACACACACACACAC 409
Qy 136 g-----Le 137
Db 408 GCCCCATGAGAGTGGCTGGGAAACAGGGGACAGAGATGGAGGAGAGTCTGATGATTT 349
Qy 137 uProHis-ThrLeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsn 157
Db 348 ACCCAAAACCTCTACAAATGTGCCAAATCAACTTCGCTGAGATGAGAGTGTGCTCAAG 289
Qy 157 lAtyTrpGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyIleCys 177
Db 288 TCTACCCAGAAAGATCATCTGACATGATGTTGTGTGGCGGACCAAAAGAGGTGGCAAG 229
Qy 177 sPserCysGlnGlyAspSerGlyIleProLeuValCysAsnGlnSerLeuGlnGlyIle 197
Db 228 ACTCCTGTGAGAGGTGACCTCTGGGGGCCCTGTGTGTGTAACAGAACTGTATGACATCG 169
Qy 197 lSerTrpGlyGlnAspProCysAlaIleThrArgIleCysProGlyValIleThrIleCys 217
Db 168 TCTCTGTGGGAGACTTCCCATGTGGGCAACCTGACCGGCGCTGTGTACACACCGTGTCT 109
Qy 217 yLysTrpValAspTrpIleGlnGlnIleThrMetIleCys 228
Db 108 CAAGTACGCTCTGTGATCCGTGAACAAATCCGA 74

RESULT 13
US-08-768-859A-9
: Sequence 9, Application US/08768859A
: Patent No. 6013471
: GENERAL INFORMATION:
: APPLICANT: Tindall, Donald J.
: APPLICANT: Young, Charles Y.F.
: APPLICANT: Saedi, Mohammed S.
: TITLE OF INVENTION: DNA Encoding HK2 Variant Polypeptides
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
: STREET: P.O. Box 2938
: CITY: Minneapolis
: STATE: MN
: COUNTRY: USA
: ZIP: 55402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/768,859A
: FILING DATE: 17-DECEMBER-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Woessner, Warren D.
: REGISTRATION NUMBER: 30,440
: REFERENCE/DOCKET NUMBER: 545,002US3

```

```

1 TELECOMMUNICATION INFORMATION
2 TELEPHONE: 612-339-0331
3 TELEFAX: 612-339-3061
4 INFORMATION FOR SEQ ID NO: 9:
5 SEQUENCE CHARACTERISTICS:
6 LENGTH: 766 base pairs
7 TYPE: nucleic acid
8 STRANDEDNESS: double
9 TOPOLOGY: linear
10 MOLECULE TYPE: cDNA
11 FEATURE:
12 NAME/KEY: CDS
13 LOCATION: 1..732
14 US-08-768-8594-9

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Db 259 AGCCTTGAGACATCAAGCCTTAGACAGATGACAGCTCCAGCCATGACCTCAGCTG 318
Qy 94 VallysMetAlaSerProValSerIleThrTrpAlaValArgProLeuThrLeuSerSer 113
Db 319 CTCGCCCTGTGACAGCTGCCAGATCAAGATGTTGGAAGGCTCCTGGCCCTGCCACAC 378
Qy 114 ArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrPglySerThrSerPro 133
Db 379 CAGGAGCCAGACACTGGGAGCCACTGCTACGCTCAGGCTGGGGCAGCATCGAACAGAG 438
Qy 134 GlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIleGlnHisGlnLys 153
Db 439 GAGTCTTGCCGCCAGAGAGCTTCAGTGTGAGCTGCATCTCTCCATACATGACATG 498
Qy 154 CysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnLys 173
Db 499 TGTGCTAGAGCTTACTCTGAGAAGGTGACAGATCATGTTGTGTGGCTCTGGACA 558
Qy 174 GlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeu 193
Db 559 GGTGGTAAAGACACTTGTGGGGGTATCTGGGGCTCCACTGTCTGTAATGCTGCT 618
Qy 194 GlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyr 213
Db 619 CAAGGTATCACAATCATGAGGGGCTGAGGCTGATGCTGCTGAAAGCCTCTGCTGTA 678
Qy 214 ThrLysValCysLysTyrValAspTrpIleGlnIuThrMetLysAsn 230
Db 679 ACCAAGGTGTCATTACCGGAAGTGATCAAGACACCATCGACGCCAAC 729

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RESULT 15
US-08-622-046B-17
Sequence 17, Application US/08622046B
Patent No. 6103237

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GENERAL INFORMATION:

```

APPLICANT: Saedi, Mohammed S.
APPLICANT: Mikolajczyk, Stephen D.
TITLE OF INVENTION: Stable Variant HK2 Polypeptide
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Schwegman, Lundberg, Moesner & Kluch, P.A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

```

COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/622.046B
FILING DATE: 26-MARCH-1996
CLASSIFICATION: 514

```

ATTORNEY/AGENT INFORMATION:

```

NAME: Moesner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 476.001US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6903
TELEFAX: 612-339-3061

```

INFORMATION FOR SEQ ID NO: 17:

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SEQUENCE CHARACTERISTICS:
LENGTH: 766 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..732
US-08-622-046B-17

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Alignment Scores:
Pred. No.: 1,32e-52 Length: 766
Score: 582.50 Matches: 107
Percent Similarity: 62.87% Conservative: 42
Best Local Similarity: 45.15% Mismatches: 81
Query Match: 46.12% Indels: 7
DB: 3 Gaps: 1

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US-09-856-320A-2_COPY_53_282 (1-230) x US-08-622-046B-17 (1-766)

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Qy 1 ArgIleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPhe 20
Db 19 CGGATTGTGGAGGCTGGGAGTGTGAGAAGCATTCCTCCAAACCTGGCAGGTCTGTAC 78
Qy 21 GlnLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 40
Db 79 AGTCATGATGGGCAACACTGTGGGGGTCTCGTGCAACCCCACTGGGTCTCACAGCT 138
Qy 41 AlaHisCysLeuLysProArgTyrIleValHisLeuGlnHisAsnLeuGlnLysGlu 60
Db 139 GCCCATTCCTTAAGAAGATGACAGGTCTGTGGCTGGGTGGGCAACACTGTTAGCCT 198
Qy 61 GlyGlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsn 80
Db 199 GAAAGACAGGCGCAGAGGCTCCCTGTCAAGCCACACTTCCACACCCGCTTACAAATAG 258
Qy 81 SerLeu-----ProAsnLysAspHisArgAsnAspIleMetLeu 93
Db 259 AGCCTTGAGACATCAAGCCTTAGACAGATGAGACTCCAGCCATGACTCATAGCTG 318
Qy 94 VallysMetAlaSerProValSerIleThrTrpAlaValArgProLeuThrLeuSerSer 113
Db 319 CTCGCCCTGTGACAGCTGCCAGATCAAGATGTTGGAAGGCTCCTGGCCCTGCCACAC 378
Qy 114 ArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrPglySerThrSerPro 133
Db 379 CAGGAGCCAGACACTGGGAGCCACTGCTACGCTCAGGCTGGGGCAGCATCGAACAGAG 438
Qy 134 GlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIleGlnHisGlnLys 153
Db 439 GAGTCTTGCCGCCAGAGAGCTTCAGTGTGAGCTGCATCTCTCCATACATGACATG 498
Qy 154 CysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnLys 173
Db 499 TGTGCTAGAGCTTACTCTGAGAAGGTGACAGATCATGTTGTGTGGCTCTGGACA 558
Qy 174 GlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeu 193
Db 559 GGTGGTAAAGACACTTGTGGGGGTATCTGGGGCTCCACTGTCTGTAATGCTGCT 618
Qy 194 GlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyr 213
Db 619 CAAGGTATCACAATCATGAGGGGCTGAGGCTGATGCTGCTGAAAGCCTCTGCTGTA 678
Qy 214 ThrLysValCysLysTyrValAspTrpIleGlnIuThrMetLysAsn 230
Db 679 ACCAAGGTGTCATTACCGGAAGTGATCAAGACACCATCGACGCCAAC 729

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Search completed: December 23, 2002, 16:03:53
Job time : 73 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 13:07:57 ; Search time 80 Seconds
(without alignments)
383.096 Million cell updates/sec

Title: US-09-856-320A-2_COPY_53_282
Perfect score: 1363

Sequence: 1 RIIGFECKPHSQPWQALF.....GVYTKVCKYVDWDIQTMMKN 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

1. A.Geneseq.101002.*

2. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1980..DAT.*

3. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1981..DAT.*

4. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1982..DAT.*

5. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1983..DAT.*

6. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1984..DAT.*

7. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1985..DAT.*

8. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1986..DAT.*

9. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1987..DAT.*

10. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1988..DAT.*

11. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1989..DAT.*

12. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1990..DAT.*

13. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1991..DAT.*

14. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1992..DAT.*

15. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1993..DAT.*

16. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1994..DAT.*

17. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1995..DAT.*

18. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1996..DAT.*

19. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1997..DAT.*

20. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1998..DAT.*

21. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA1999..DAT.*

22. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA2000..DAT.*

23. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA2001..DAT.*

24. /SID52./gcgcdata./geneseq./geneseqp./emb1./AA2002..DAT.*

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1263	100.0	250	21	AAB21325	Human TRIP. Homo
2	1263	100.0	250	21	AAV99390	Human Prol279 (UNC
3	1263	100.0	250	22	ABB50479	Human secreted pro
4	1263	100.0	250	22	AAU12424	Human Prol279 pol
5	1263	100.0	250	22	AAB66139	Protein of the inv
6	1263	100.0	250	23	ABG61816	Prostate cancer-as
7	1263	100.0	250	23	ABB95526	Human angiogenesis
8	1263	100.0	250	23	ABB84920	Human Prol279 pro
9	1263	100.0	250	23	AAU83684	Human PRO protein
10	1263	100.0	282	20	AAV42439	CASB12 amino acid

11	1363	100.0	282	21	AAAB1712	Human serine protease
12	1263	100.0	282	21	AAAY336	A human prostate-a
13	1257	99.5	281	20	AAV42440	CASB12 polypeptide
14	1240.5	99.2	275	21	AAAB1714	Human serine protease
15	1236	97.9	228	21	AAAB21312	Human TLP. Homo
16	1233	97.6	250	20	AAV36093	Extended human sec
17	1232	97.5	248	22	AAE08017	Human PS13 consen
18	1221.5	96.7	289	21	AAAB36483	Fusion gene with h
19	1221.5	96.7	289	22	AAAB67543	Amino acid sequenc
20	1067	84.5	276	21	AAAB1713	Mouse serine prote
21	739	58.5	250	21	AAAB21298	Human KLK-L3 prote
22	739	58.5	251	22	AAU16971	Human novel secret
23	737	58.4	247	22	AAU23217	Novel human enzyme
24	734.5	58.2	296	21	AAAB21297	Human KLK-L3 prote
25	719	56.9	247	22	AAU86677	Novel human connect
26	719	56.9	247	22	AAU23752	Novel human enzyme
27	719	56.9	247	22	AAU17043	Human novel secret
28	690	54.6	275	21	AAAB21311	Human neuropilin
29	686	54.3	260	17	AAAM10694	Human recombinant
30	686	54.3	260	18	AAAM12393	Mouse neuropilin pr
31	686	54.3	260	23	AAAB57219	Mouse ischemic co
32	684	54.2	256	23	AAU79390	Novel human kalik
33	684	54.2	320	23	AAE19166	Human proteinase, PR
34	684	54.2	320	23	AAU83732	Amino acid sequenc
35	683	54.1	260	20	AAV41744	Human PRO322 prote
36	683	54.1	260	20	AAV37852	Human serine prote
37	683	54.1	260	20	AAV03220	Amino acid sequenc
38	683	54.1	260	20	AAW87703	A human serine pro
39	683	54.1	260	21	AAAB21322	Human neuropilin
40	683	54.1	260	21	AAAB44300	Human PRO322 (UNO2
41	683	54.1	260	21	AAV51131	Human neuropilin pr
42	683	54.1	260	22	AAAG23373	Novel human diagno
43	683	54.1	260	22	AAU13369	Human PRO322 polyp
44	683	54.1	260	22	AAU53087	Human angiogenesis
45	683	54.1	260	23	AAAB55458	Human angiogenesis

ALIGNMENTS

XX	RESULT 1
XX	ABAB21325
XX	ABAB21325 standard; protein; 250 AA.
XX	ABAB21325;
XX	02-FEB-2001 (first entry)
XX	Human TLSP.
XX	Human; K1K-L1; K1K-L2; K1K-L3; K1K-L4; K1K-L5; K1K-L6; TLSP;
XX	trypsin-like serine protease; kallikrein-like protein; serine protease;
XX	cytostatic; cancer; prostate cancer.
XX	Homo sapiens.
XX	WO2000053776-A2.
XX	14-SEP-2000.
XX	09-MAR-2000; 2000WO-CA00258.
XX	11-MAR-1999; 99US-0124260.
XX	01-APR-1999; 99US-0127386.
XX	21-JUL-1999; 99US-0144919.
XX	(MOUN) MOUNT SINAI HOSPITAL.
XX	Yousef GM, Diamandis EP;
XX	WPI; 2000-567440/55.
XX	New kallikrein-like (K1K-L) proteins for diagnosing and treating K1K-L

PT protein mediated disorders, especially cancer. -
XX
PS Example 5; Fig 27; 184pp; English.
XX
CC The present sequence is human trypsin-like serine protease (TLSP), a
CC member of the serine protease family. Kallikreins and
CC kallikrein-like proteins are a subgroup of the serine protease enzyme
CC family. They catalyse the selective cleavage of specific polypeptide
CC precursors to release peptides with potent biological activity. Nucleic
CC acids encoding kallikrein-like proteins KLK-11, KLK-12, KLK-13, KLK-14,
CC KLK-15 and KLK-16 have been isolated. The proteins are useful in the
CC treatment, monitoring and diagnosis of cancers, especially prostate
CC cancer. They can also be used to identify a substance that can associate
CC with or mediate the biological activity of the proteins. Antibodies can
CC be used to treat conditions mediated by the kallikrein-like proteins.
XX
SQ Sequence 250 AA;

Query Match 100.0%; Score 1263; DB 21; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-113;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIIFGFECKRHSOPWQALFEKTRLLCGATLIAPRWLLTFAHCLKPRYIYHLOGHNOKE 60
Db 21 RIIFGFECKRHSOPWQALFEKTRLLCGATLIAPRWLLTFAHCLKPRYIYHLOGHNOKE 80
QY 61 EGCEQRTFATESFPHPGFNNSLPKNRHNDIMLVKASPVSIWAVRPLTSSRCVTAGT 120
Db 81 EGCEQRTFATESFPHPGFNNSLPKNRHNDIMLVKASPVSIWAVRPLTSSRCVTAGT 140
QY 121 SCLISGSGTSSPOLRLPHRLRCANITIIHOCENAYPKNIDPTWCASVOEGKRSQC 180
Db 141 SCLISGSGTSSPOLRLPHRLRCANITIIHOCENAYPKNIDPTWCASVOEGKRSQC 200
QY 181 GDSGGPLVQNSLOGISMGODPCATIRKPGYTKVCKYDWMIOETKNN 230
Db 201 GDSGGPLVQNSLOGISMGODPCATIRKPGYTKVCKYDWMIOETKNN 250

RESULT 2
AAV99390
ID AAV99390 standard; Protein; 250 AA.
XX
AC AAV99390;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1279 (UNC649) amino acid sequence SEQ ID NO:170.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW Transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS Homo sapiens.
XX
PN WO200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US20111.
XX
PR 01-SEP-1998; 98US-0098716.
PR 01-SEP-1998; 98US-0098749.
PR 01-SEP-1998; 98US-0098750.
PR 02-SEP-1998; 98US-0098803.
PR 02-SEP-1998; 98US-0098821.
PR 02-SEP-1998; 98US-0098843.
PR 09-SEP-1998; 98US-0099536.
PR 09-SEP-1998; 98US-0099596.
PR 09-SEP-1998; 98US-0099598.
PR 09-SEP-1998; 98US-0099602.
PR 09-SEP-1998; 98US-0099642.
PR 10-SEP-1998; 98US-0099741.
PR 10-SEP-1998; 98US-0099754.

PR 10-SEP-1998; 98US-0099763.
PR 10-SEP-1998; 98US-0099792.
PR 10-SEP-1998; 98US-0099808.
PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099815.
PR 10-SEP-1998; 98US-0099816.
PR 15-SEP-1998; 98US-0100385.
PR 15-SEP-1998; 98US-0100388.
PR 15-SEP-1998; 98US-0100390.
PR 16-SEP-1998; 98US-0100584.
PR 16-SEP-1998; 98US-0100627.
PR 16-SEP-1998; 98US-0100661.
PR 16-SEP-1998; 98US-0100662.
PR 16-SEP-1998; 98US-0100664.
PR 17-SEP-1998; 98US-0100683.
PR 17-SEP-1998; 98US-0100684.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.
PR 17-SEP-1998; 98US-0100919.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 23-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102330.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102965.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105000.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.
PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.

PR 27-OCT-1998; 98US-0105882.
 PR 27-OCT-1998; 98US-0106062.
 PR 28-OCT-1998; 98US-0106023.
 PR 28-OCT-1998; 98US-0106029.
 PR 28-OCT-1998; 98US-0106030.
 PR 28-OCT-1998; 98US-0106032.
 PR 28-OCT-1998; 98US-0106033.
 PR 28-OCT-1998; 98US-0106178.
 PR 29-OCT-1998; 98US-0106248.
 PR 29-OCT-1998; 98US-0106384.
 PR 30-OCT-1998; 98US-0106500.
 PR 30-OCT-1998; 98US-0106464.
 PR 03-NOV-1998; 98US-0106856.
 PR 03-NOV-1998; 98US-0106902.
 PR 03-NOV-1998; 98US-0106905.
 PR 03-NOV-1998; 98US-0106919.
 PR 03-NOV-1998; 98US-0106932.
 PR 03-NOV-1998; 98US-0106934.
 PR 10-NOV-1998; 98US-0107783.
 PR 17-NOV-1998; 98US-0108775.
 PR 17-NOV-1998; 98US-0108779.
 PR 17-NOV-1998; 98US-0108787.
 PR 17-NOV-1998; 98US-0108788.
 PR 17-NOV-1998; 98US-0108801.
 PR 17-NOV-1998; 98US-0108802.
 PR 17-NOV-1998; 98US-0108806.
 PR 17-NOV-1998; 98US-0108807.
 PR 17-NOV-1998; 98US-0108867.
 PR 17-NOV-1998; 98US-0108925.
 PR 18-NOV-1998; 98US-0108848.
 PR 18-NOV-1998; 98US-0108849.
 PR 18-NOV-1998; 98US-0108850.
 PR 18-NOV-1998; 98US-0108851.
 PR 18-NOV-1998; 98US-0108852.
 PR 18-NOV-1998; 98US-0108858.
 PR 18-NOV-1998; 98US-0108904.
 PR (GETH) GENENTECH INC.
 PA Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
 PI WPI: 2000-237871/20.
 DR N-PSDB: AAA37072.
 XX
 XX New mammalian DNA sequences encoding transmembrane, receptor or
 PT secreted PRO polypeptides, useful for screening of potential peptide or
 PT small molecule inhibitors of the relevant receptor/ligand interactions
 PS Claim 12; Fig 102; 773pp; English.
 XX
 CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
 CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding them have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA3730 represent
 CC PCR primers and hybridisation probes used in the isolation of the PRO
 CC polypeptides from the present invention.
 XX
 SO Sequence 250 AA;
 Query Match 100.0%; Score 1263; DB 21; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-113;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 SCLISGSGSTSSPOLRLPHRLRCANITLIEHQKCEANAPGNITDTMCASVOEGKDSQ 180
 Db 141 SCLISGSGSTSSPOLRLPHRLRCANITLIEHQKCEANAPGNITDTMCASVOEGKDSQ 200
 QY 181 GDSGGLVNCNSLOGIISWGDPACITRKPGYVYTVCKCYVMIOETMKN 230
 Db 201 GDSGGLVNCNSLOGIISWGDPACITRKPGYVYTVCKCYVMIOETMKN 250
 RESULT 3
 ID ABB50479 standard; Protein: 250 AA.
 AC ABB50479;
 XX
 XX 07-FEB-2002 (first entry)
 DE Human secreted protein encoded by gene 179 SEQ ID NO:427.
 XX
 KW Human; secreted protein; immunomodulatory; antifibrotic; anti-HIV;
 KW dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 KW cyrostatic; cardiant; vascular; anti-angiogenic; ophthalmological;
 KW neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnerary;
 KW multiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
 KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
 KW human immunodeficiency virus; hyperproliferative disorder; wound healing;
 KW Gaucher's disease; cardiovascular disease; scleritar syndrome; chemotaxis;
 KW Chaga's cardiomyopathy; coronary arteriosclerosis; angiocentric disorder;
 KW corneal graft neovascularisation; diabetic retinopathy; regeneration;
 KW neurological disorder; Huntington's chorea; Alzheimer's disease;
 KW Parkinson's disease; infectious disease.
 XX
 OS Homo sapiens.
 XX
 PN W0200162891-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 21-FEB-2001; 2001WO-US05614.
 XX
 PR 24-FEB-2000; 2000US-184836P.
 PR 29-MAR-2000; 2000US-193170P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI NI J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;
 PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
 PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrle AM, Fan P;
 PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;
 PI Zeng Z, Greene JM;
 XX
 DR WPI: 2001-625724/72.
 DR N-PSDB: ABA83372.
 XX
 XX Nucleic acids encoding 207 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -
 XX
 XX Claim 11; Page 1181-1182; 1533pp; English.
 XX
 CC ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
 CC activities based on the tissues and cells the genes are expressed in.
 CC Example of these activities include: immunomodulatory; antisclerotic;
 CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 CC anti-HIV; cyostatic; cardiant; anti-angiogenic; ophthalmological;
 CC neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular;
 CC antiparkinsonian; antimicrobial; and vulnerary. (I) and (II) can be used
 CC in gene therapy and vaccine production. (I) and (II) can be used in the
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and

CC Gaucher's disease), cardiovascular diseases (e.g. Sclimtar syndrome,
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiodysplastic
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA8185 to
 CC ABA8193 and ABA85000 represent sequences used in the exemplification of
 CC the present invention.
 CC
 XX
 SQ Sequence 250 AA;
 Query Match 100.0%; Score 1263; DB 22; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-113;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIIRGFECCKPHSQPQWQALFEKTRLLCGATLIAPRWLLTAHCLKPRYIYHLOHNLQKE 60
 DB 21 RIIRGFECCKPHSQPQWQALFEKTRLLCGATLIAPRWLLTAHCLKPRYIYHLOHNLQKE 80
 QY 61 EGCBOITRATESFPHGFNNSLPNKDRNDIMLVKMA SPVSIWAVRPLTLSSRCVTAGT 120
 DB 81 EGCBOITRATESFPHGFNNSLPNKDRNDIMLVKMA SPVSIWAVRPLTLSSRCVTAGT 140
 QY 121 SCLISGSGSTSSPOLRLPHTLRCA NITIIIEHOKCENAPGNTITDTWVCASVQEGGKDSQ 180
 DB 141 SCLISGSGSTSSPOLRLPHTLRCA NITIIIEHOKCENAPGNTITDTWVCASVQEGGKDSQ 200
 QY 181 GDSGGPLVCMNSLOGIISWGODPCAITRKPGVYTKCKYVDWIOETMKN 230
 DB 201 GDSGGPLVCMNSLOGIISWGODPCAITRKPGVYTKCKYVDWIOETMKN 250
 RESULT 4
 AAU12424
 ID AAU12424 standard; Protein: 250 AA.
 XX
 AC AAU12424;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human PRO1279 polypeptide sequence.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 PE 01-DEC-2000; 2000MO-US32678.
 XX
 PR 01-DEC-1999; 99MO-US28301.
 PR 01-DEC-1999; 99MO-US28634.
 PR 02-DEC-1999; 99MO-US28551.
 PR 02-DEC-1999; 99MO-US28564.
 PR 02-DEC-1999; 99MO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99MO-US30095.
 PR 20-DEC-1999; 99MO-US30911.
 PR 20-DEC-1999; 99MO-US30999.
 PR 30-DEC-1999; 99MO-US31243.
 PR 06-JAN-2000; 2000MO-US00377.
 PR 06-JAN-2000; 2000MO-US00378.
 PR 11-FEB-2000; 2000MO-US03565.
 PR 18-FEB-2000; 2000MO-US04341.
 PR 18-FEB-2000; 2000MO-US04342.
 PR 22-FEB-2000; 2000MO-US04414.
 PR 24-FEB-2000; 2000MO-US04914.
 PR 24-FEB-2000; 2000MO-US05004.

PR 01-MAR-2000; 2000MO-US05601.
 PR 20-MAR-2000; 2000MO-US07317.
 PR 21-MAR-2000; 2000MO-US07532.
 PR 30-MAR-2000; 2000MO-US08439.
 PR 17-MAY-2000; 2000MO-US13705.
 PR 22-MAY-2000; 2000MO-US14042.
 PR 30-MAY-2000; 2000MO-US14941.
 PR 02-JUN-2000; 2000MO-US15264.
 PR 10-NOV-2000; 2000MO-US30873.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Baker KP, Beresini M, DeGeorge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart JA, Tamas D, Watanabe CK, Wood WI, Zhang Z;
 DR WPT: 2001-408281/43.
 XX N-P-SDB; AAS21496.
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX
 PS Claim 12; Fig 506; 813p; English.
 XX
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX
 XX
 SQ Sequence 250 AA;
 Query Match 100.0%; Score 1263; DB 22; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-113;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIIRGFECCKPHSQPQWQALFEKTRLLCGATLIAPRWLLTAHCLKPRYIYHLOHNLQKE 60
 DB 21 RIIRGFECCKPHSQPQWQALFEKTRLLCGATLIAPRWLLTAHCLKPRYIYHLOHNLQKE 80
 QY 61 EGCBOITRATESFPHGFNNSLPNKDRNDIMLVKMA SPVSIWAVRPLTLSSRCVTAGT 120
 DB 81 EGCBOITRATESFPHGFNNSLPNKDRNDIMLVKMA SPVSIWAVRPLTLSSRCVTAGT 140
 QY 121 SCLISGSGSTSSPOLRLPHTLRCA NITIIIEHOKCENAPGNTITDTWVCASVQEGGKDSQ 180
 DB 141 SCLISGSGSTSSPOLRLPHTLRCA NITIIIEHOKCENAPGNTITDTWVCASVQEGGKDSQ 200
 QY 181 GDSGGPLVCMNSLOGIISWGODPCAITRKPGVYTKCKYVDWIOETMKN 230
 DB 201 GDSGGPLVCMNSLOGIISWGODPCAITRKPGVYTKCKYVDWIOETMKN 250
 RESULT 5
 AAB66139
 ID AAB66139 standard; protein: 250 AA.

```
XX AC AAB6139;
XX DT 02-APR-2001 (first entry)
XX DE Protein of the invention #51.
XX KW Secreted; transmembrane; gene therapy.
XX OS Unidentified.
XX PN WO200078961-A1.
XX PD 28-DEC-2000.
XX PF 18-FEB-2000; 2000WO-US04342.
XX PR 23-JUN-1999; 99US-0141037.
XX PR 20-JUL-1999; 99US-0144758.
XX PR 26-JUL-1999; 99US-0145698.
XX PR 01-SEP-1999; 99WO-US20111.
XX PR 29-OCT-1999; 99US-0162506.
XX PR 30-NOV-1999; 99WO-US28313.
XX PR 02-DEC-1999; 99WO-US28551.
XX PR 16-DEC-1999; 99WO-US30095.
XX PR 05-JAN-2000; 2000WO-US00219.
XX PR 06-JAN-2000; 2000WO-US00376.
XX PA (GETH ) GENENTECH INC.
XX PI Baker KP, Bolstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
XX PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;
XX PI Watanabe CK, Williams PM, Wood WI;
XX DR WPI: 2001-071395/08.
XX PT Secreted and transmembrane proteins and nucleic acids designated PRO,
XX PT useful as hybridization probes, in chromosome and gene mapping and gene
XX PT therapy -
XX PS Claim 1; Fig 102; 787pp; English.
XX CC The present invention relates to secreted and transmembrane proteins.
XX CC These proteins and the DNA encoding them may be used as hybridization
XX CC probes, in chromosome and gene mapping and in the generation of
XX CC anti-sense RNA and DNA. They may also be used to generate either
XX CC transgenic animals or knockout animals which are in turn useful for
XX CC development and screening of therapeutically useful reagents.
XX CC The nucleic acids may also be used in gene therapy.
XX SQ Sequence 250 AA;
SQ Query Match 100.0%; Score 1263; DB 22; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-113;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIINGFECKPHSOPQOALFEKTRILCGATLIAPRWLITAAHCKPRIYHIGOHNL0KE 60
DB 21 RIINGFECKPHSOPQOALFEKTRILCGATLIAPRWLITAAHCKPRIYHIGOHNL0KE 80
QY 61 EGCETRTATSFPHPGFNNSLPNKDHRNDIMLVKMASPVSIITWAVRPLTLSSRCVTAGT 120
DB 81 EGCETRTATSFPHPGFNNSLPNKDHRNDIMLVKMASPVSIITWAVRPLTLSSRCVTAGT 140
QY 121 SCLISGMSSTSPOLRLPHTRRCANITITIEHOKCENAPGNTITPMWCAV0EGGKDSQ 180
DB 141 SCLISGMSSTSPOLRLPHTRRCANITITIEHOKCENAPGNTITPMWCAV0EGGKDSQ 200
QY 181 GDSGSPVLCNCSL0GIISMGODPCATIRKPGVYTRKVCXYVMIOETMKN 230
DB 201 GDSGSPVLCNCSL0GIISMGODPCATIRKPGVYTRKVCXYVMIOETMKN 250
```

```
RESULT 6
ABG61816
ID ABG61816 standard; Protein; 250 AA.
XX AC ABG61816;
XX DT 15-AUG-2002 (first entry)
XX DE Prostate cancer-associated protein #17.
XX KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
XX OS Mammalia.
XX PN WO200230268-A2.
XX PD 18-APR-2002
XX PF 12-OCT-2001; 2001WO-US32045.
XX PR 13-OCT-2000; 2000US-0687576.
XX PR 08-DEC-2000; 2000US-0733288.
XX PR 08-DEC-2000; 2000US-0733742.
XX PR 24-JAN-2001; 2001US-263957P.
XX PR 16-MAR-2001; 2001US-276791P.
XX PR 16-MAR-2001; 2001US-276888P.
XX PR 06-APR-2001; 2001US-281922P.
XX PR 24-APR-2001; 2001US-286214P.
XX PR 30-APR-2001; 2001US-0847046.
XX PR 04-MAY-2001; 2001US-288589P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX PI Glish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX DR WPI: 2002-471335/50.
XX DR N-PSDB; ABK92131.
XX PT Detecting a prostate cancer-associated transcript in a cell in a
XX PT patient, useful for diagnosing prostate cancer (PC) or screening
XX PT modulators of PC, by determining if prostate cancer-associated genes
XX PT are expressed in a prostate tissue -
XX PS Claim 27; Page 314; 436pp; English.
XX CC The present invention relates to methods of detecting a prostate
XX CC cancer-associated transcript in a cell from a patient. The method
XX CC comprises contacting a biological sample from the patient with
XX CC prostate cancer-associated polynucleotides (designated PC genes) that
XX CC selectively hybridise to a sequence that is at least 80% identical
XX CC to them. The prostate cancer-associated polynucleotide sequences
XX CC are differentially expressed in prostate tumour tissue or in
XX CC prostate cancer and are derived from the tissues of various
XX CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
XX CC The methods of the invention are useful for diagnosing and treating
XX CC prostate cancer in mammals. The prostate cancer-associated genes are
XX CC useful for diagnosing or treating prostate cancer, as well as for
XX CC identifying modulators of prostate cancer or agents that inhibit
XX CC prostate cancer. The nucleic acid sequences are particularly useful
XX CC in gene therapy, as a vaccine or in antisense applications.
XX CC ABG61800-ABG61944 represent prostate cancer-associated proteins.
XX SQ Sequence 250 AA;
SQ Query Match 100.0%; Score 1263; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-113;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIINGFECKPHSOPQOALFEKTRILCGATLIAPRWLITAAHCKPRIYHIGOHNL0KE 60
DB 21 RIINGFECKPHSOPQOALFEKTRILCGATLIAPRWLITAAHCKPRIYHIGOHNL0KE 80
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QY 61 EGCQOTRATESFPHPGNNSLPNKDHNDIMLVKMASPVSTWAVRPLTLSSRCVTAGT 120
    |||
Db 81 EGCQOTRATESFPHPGNNSLPNKDHNDIMLVKMASPVSTWAVRPLTLSSRCVTAGT 140
QY 121 SCLISGSGSTSSPOLRPLHTLRCAANTITIEHOKCENAYPGNITDPMVCASVQEGGKDSQC 180
    |||
Db 141 SCLISGSGSTSSPOLRPLHTLRCAANTITIEHOKCENAYPGNITDPMVCASVQEGGKDSQC 200
QY 181 GDSGGPLVCNOSLQGIISWGDPCAITRKPGVYTKCKYVWIDQETMKN 230
    |||
Db 201 GDSGGPLVCNOSLQGIISWGDPCAITRKPGVYTKCKYVWIDQETMKN 250

RESULT 7
ABB95526
ID ABB95526 standard; Protein; 250 AA.
XX
AC ABB95526;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related protein PRO1279 SEQ ID NO: 208.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiomy; cytosolic; antiangiogenic; hypotensive; vulnary;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN MO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21735.
XX
PR 20-JUL-2000; 2000US-219555P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 28-JUN-2001; 2001WO-US00000.

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```

XX (GETH ) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PAON/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WJ, Ye W;
PI
XX WPI: 2002-171999/22.
DR N-PSDB; ABL95664.
XX
PS Claim 11; Fig 208; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention.
XX
SO Sequence 250 AA;
XX
Query Match 100.0%; Score 1263; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-113;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIIFGFECKRHSOPWQALFEKTRLLCGATLIPRMLTAHCLKPRYVHLOHNLQKE 60
    |||
Db 21 RIIFGFECKRHSOPWQALFEKTRLLCGATLIPRMLTAHCLKPRYVHLOHNLQKE 80
QY 61 EGCQOTRATESFPHPGNNSLPNKDHNDIMLVKMASPVSTWAVRPLTLSSRCVTAGT 120
    |||
Db 81 EGCQOTRATESFPHPGNNSLPNKDHNDIMLVKMASPVSTWAVRPLTLSSRCVTAGT 140
QY 121 SCLISGSGSTSSPOLRPLHTLRCAANTITIEHOKCENAYPGNITDPMVCASVQEGGKDSQC 180
    |||
Db 141 SCLISGSGSTSSPOLRPLHTLRCAANTITIEHOKCENAYPGNITDPMVCASVQEGGKDSQC 200
QY 181 GDSGGPLVCNOSLQGIISWGDPCAITRKPGVYTKCKYVWIDQETMKN 230
    |||
Db 201 GDSGGPLVCNOSLQGIISWGDPCAITRKPGVYTKCKYVWIDQETMKN 250

RESULT 8
ABB84920
ID ABB84920 standard; Protein; 250 AA.
XX
AC ABB84920;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO1279 protein sequence SEQ ID NO: 208.
XX

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KM Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
 KM vultnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KM gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KM angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KM age-related macular degeneration; arterial restenosis; angina;
 KM rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KM lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KM wound healing; chromosome mapping; gene mapping.
 OS Homo sapiens.
 XX WO200200690-A2.
 XX 03-JAN-2002.
 XX 20-JUN-2001; 2001WO-US19692.
 XX 23-JUN-2000; 2000US-213637P.
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854280.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerlitsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
 XX
 DR WPI; 2002-090516/12.
 DR N-PSDB; ABL88175.
 XX
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 PS Claim 11; Fig 208; 565pp; English.
 XX
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cyostatic,
 CC antiangiogenic, hypotensive, vultnary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides
 CC proteins, agonists and antagonists are useful for treating or diagnosing

CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
 CC probes used in the exemplification of the present invention.
 XX
 SQ Sequence 250 AA;
 Query Match 100.0%; Score 1263; DB 23; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-113;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIIRGFECCKPHSOPWQAALEFKETLLGATLLARWLLTAHCKLPRIYHGLGHNLOKE 60
 DB 21 RIIRGFECCKPHSOPWQAALEFKETLLGATLLARWLLTAHCKLPRIYHGLGHNLOKE 80
 QY 61 EGCQOTRATFSPHPGFNNSLPKNDRNDIMLVKMA SPVITWAVRPLTSSRCYTAGT 120
 DB 81 EGCQOTRATFSPHPGFNNSLPKNDRNDIMLVKMA SPVITWAVRPLTSSRCYTAGT 140
 QY 121 SCLISGWSTSSPOLRLPHRLRCANITITIEHOKCENAPGNITDTVMCASVOEGKDSQC 180
 DB 141 SCLISGWSTSSPOLRLPHRLRCANITITIEHOKCENAPGNITDTVMCASVOEGKDSQC 200
 QY 181 GDSSGPLVCNOSLOGIISWQODPCATIRKRGVYTKVKYDWMIOETKNN 230
 DB 201 GDSSGPLVCNOSLOGIISWQODPCATIRKRGVYTKVKYDWMIOETKNN 250
 RESULT 9
 ID ABL883684 standard; Protein: 250 AA.
 XX
 AC AAU83684;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human PRO protein, Seq ID No 186.
 XX
 XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KM breast cancer; prostate tumour; rectal tumour; liver tumour;
 KM pericyte cell proliferation; chondrocyte cell proliferation;
 KM tumour necrosis factor-alpha.
 OS Homo sapiens.
 XX
 PN WO200208288-A2.
 XX
 PD 31-JAN-2002.
 XX
 XX 29-JUN-2001; 2001WO-US21066.
 PF
 XX 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.

PR 20-DEC-2000; 2000MO-US34956.
PR 28-FEB-2001; 2001MO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001MO-US17092.
XX
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2002-172001/22.
DR N-PSDB; ABR33628.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour -
XX
XX Claim 11: Figure 186; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AA083592-AA083713 represent human PRO
CC protein sequences of the invention.
XX
XX Sequence 250 AA:
SQ
Query Match 100.0%; Score 1263; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-113;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIIRGFECKRHSQPMQAALEKTRLLCGATLIPRWLITRAHCLKPRYIVHLCQHNLQKE 60
DB 21 RIIRGFECKRHSQPMQAALEKTRLLCGATLIPRWLITRAHCLKPRYIVHLCQHNLQKE 80
QY 61 EGCEQRTATSEFPHPGFNNSLPNKDRNDIMLVKMASPVSTIWAARPLTLSSRCVTAGT 120
DB 81 EGCEQRTATSEFPHPGFNNSLPNKDRNDIMLVKMASPVSTIWAARPLTLSSRCVTAGT 140
QY 121 SCLISGWSSTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDTWVCASVQSGKDSQ 180
DB 141 SCLISGWSSTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDTWVCASVQSGKDSQ 200
QY 181 GDSGGPLVCNOSLOGIISWGQDPCATRRKPGVYTKVKYVDWIOETMKNK 230
DB 201 GDSGGPLVCNOSLOGIISWGQDPCATRRKPGVYTKVKYVDWIOETMKNK 250
RESULT 10
AA42439
ID AAY42439 standard; Protein; 282 AA.
XX
XX AAY42439;
XX
XX 08-DEC-1999 (first entry)
XX
XX CASB12 amino acid sequence.
XX
XX neuropeptin; cancer; assay; inhibitor; serine protease; immunogenic;
KW autoimmune disease.
XX

OS Homo sapiens.
XX
XX WO9949055-A1.
XX
XX 30-SEP-1999.
XX
XX 17-MAR-1999; 99WO-EP01894.
XX
XX 20-MAR-1998; 98GB-0006095.
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Bruck CEM, Cassart J, Coche T, Vinals-Bassols C;
PI WPI; 1999-580450/49.
DR N-PSDB; AA222638.
XX
XX New human serine protease CASB12, for treatment, prevention and
PT diagnosis of cancer and autoimmune diseases -
PT
XX
XX Claim 3: Page 48; 58pp; English.
XX
XX This is the amino acid sequence of the CASB12 protein. The nucleotide
CC sequence of AA222638 shows homology with neuropeptin and the encoded
CC protein AA42439 is structurally related to other proteins of the
CC serine protease family, having homology and/or structural similarity
CC with neuropeptin. It is expected that as well as similar structure, these
CC proteins will also share similar biological functions and properties.
CC The CASB12 polypeptides and polynucleotides can be used to develop
CC methods for identifying agonists and antagonists/inhibitors of these
CC molecules, and thereby treating conditions associated with CASB12
CC polypeptide imbalance. The invention also provides for diagnostic assays
CC for detecting diseases associated with inappropriate CASB12 polypeptide
CC activity or levels.
CC Since CASB12 is either specifically expressed or highly over-expressed
CC in tumors compared to normal cells, the polypeptides and polynucleotides
CC of the invention are believed to be important immunogens for specific
CC prophylactic or therapeutic immunization against tumors. The
CC polypeptides and polynucleotides can therefore be targeted by antigen
CC specific immune reactions (which result in the destruction of the tumor
CC cell) or they can be used to diagnose the occurrence of tumor cells
XX
XX Sequence 282 AA:
SQ
Query Match 100.0%; Score 1263; DB 20; Length 282;
Best Local Similarity 100.0%; Pred. No. 2.4e-113;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIIRGFECKRHSQPMQAALEKTRLLCGATLIPRWLITRAHCLKPRYIVHLCQHNLQKE 60
DB 53 RIIRGFECKRHSQPMQAALEKTRLLCGATLIPRWLITRAHCLKPRYIVHLCQHNLQKE 112
QY 61 EGCEQRTATSEFPHPGFNNSLPNKDRNDIMLVKMASPVSTIWAARPLTLSSRCVTAGT 120
DB 113 EGCEQRTATSEFPHPGFNNSLPNKDRNDIMLVKMASPVSTIWAARPLTLSSRCVTAGT 172
QY 121 SCLISGWSSTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDTWVCASVQSGKDSQ 180
DB 173 SCLISGWSSTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDTWVCASVQSGKDSQ 232
QY 181 GDSGGPLVCNOSLOGIISWGQDPCATRRKPGVYTKVKYVDWIOETMKNK 230
DB 233 GDSGGPLVCNOSLOGIISWGQDPCATRRKPGVYTKVKYVDWIOETMKNK 282
RESULT 11
AAB11712
ID AAB11712 standard; Protein; 282 AA.
XX
XX AAB11712;
XX
XX 23-OCT-2000 (first entry)
XX

CC tumor-associated antigens. The nucleotide sequence of AA222638 shows
 CC homology with neuropilin and the encoded protein AAV42439 is structurally
 CC related to other proteins of the serine protease family, having homology
 CC and/or structural similarity with neuropilin. It is expected that as well
 CC as similar structure, these proteins will also share similar biological
 CC functions and properties.
 CC The CASB12 polypeptides and polynucleotides can be used to develop
 CC methods for identifying agonists and antagonists/inhibitors of these
 CC molecules, and thereby treating conditions associated with CASB12
 CC polypeptide imbalance. The invention also provides for diagnostic assays
 CC for detecting diseases associated with inappropriate CASB12 polypeptide
 CC activity or levels.
 CC Since CASB12 is either specifically expressed or highly over-expressed
 CC in tumors compared to normal cells, the polypeptides and polynucleotides
 CC of the invention are believed to be important immunogens for specific
 CC prophylactic or therapeutic immunization against tumors. The
 CC polypeptides and polynucleotides can therefore be targeted by antigen
 CC specific immune reactions (which result in the destruction of the tumor
 CC cell) or they can be used to diagnose the occurrence of tumor cells

SO Sequence 281 AA:
 Query Match 99.5%; Score 1257; DB 20; Length 281;
 Best Local Similarity 100.0%; Pred. No. 8,9e-113;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIIGFECKPHSOPWQAALFEKTRLLCGATLLAPRWLLTAAHCLKPRYIYHLCGHNLOKE 60
 DB 53 RIIGFECKPHSOPWQAALFEKTRLLCGATLLAPRWLLTAAHCLKPRYIYHLCGHNLOKE 112
 QY 61 EGCEQRTATESPFPFGNNSLPKNDHRNDIMLVKMA SPVSIWAVRPLTSSRCVTAGT 120
 DB 113 EGCEQRTATESPFPFGNNSLPKNDHRNDIMLVKMA SPVSIWAVRPLTSSRCVTAGT 172
 QY 121 SCITSGSGSSSPQLRPHRLRCANITITIEHOKCENAYPGNITDTMWCASVOEGKRSQC 180
 DB 173 SCITSGSGSSSPQLRPHRLRCANITITIEHOKCENAYPGNITDTMWCASVOEGKRSQC 232
 QY 181 GDSGGPLVCNOSLOGIISMGODPCATITRRKPGVYTKVCKYVDWIOETMKN 229
 DB 233 GDSGGPLVCNOSLOGIISMGODPCATITRRKPGVYTKVCKYVDWIOETMKN 281

RESULT 14
 AAB11714
 ID AAB11714 standard; Protein; 275 AA.
 AC AAB11714;
 DT 23-OCT-2000 (first entry)
 DE Human serine protease BSSP6 (hbSSP6) SEQ ID NO:6.
 DE XX
 KW BSSP6; serine protease; human; hbSSP6; mouse; mbSSP6; brain;
 KW diagnostic marker; antibody; transgenic animal; Alzheimer's disease;
 KW epilepsy; cancer; inflammation; infertility; pancreatitis;
 KW prostatic hypertrophy.
 OS Homo sapiens.
 PN WO200031257-A1.
 PD 02-JUN-2000.
 PF 19-NOV-1999; 99WO-JP06476.
 PR 20-NOV-1998; 98JP-0347802.
 PA (FUSO) FUSO PHARM IND LTD.
 PI Uemura H, Okui A, Kominami K, Yamaguchi N, Mitsui S;
 DR WPI; 2000-40067/34.

DR N-PSDB; AAA61765.
 XX Serine protease BSSP6, useful in detecting homologs, mutants and
 PT polymorphic variants as markers for diagnosis of Alzheimer's disease,
 PT epilepsy, cancer, inflammation, infertility and prostate hypertrophy,
 PT using blood or other tissues
 PS Claim 15; Page 77-78; 94pp; Japanese.
 XX
 CC The invention relates to novel serine proteases designated BSSP6
 CC (AAB11712-B11714), and to nucleic acids encoding them (AAA61763-A61765).
 CC The invention also relates to vectors and transformants comprising BSSP6
 CC nucleic acids; transgenic animals in which the expression level of BSSP6
 CC can be varied; and an mbSSP6 knockout mouse. The invention additionally
 CC encompasses anti-BSSP6 antibodies and methods of production of such
 CC antibodies, methods of BSSP6 detection using the antibodies, and the
 CC use of BSSP6 proteins or fragments as diagnostic markers for certain
 CC medical conditions. Nucleotides encoding BSSP6 were initially
 CC isolated in a human brain cDNA library using degenerate PCR primers
 CC (AAA61795-A61796) based on conserved regions of serine proteases. The
 CC BSSP6 serine proteases and nucleotides encoding them are useful in
 CC detecting homologues, mutants and polymorphic variants in biological
 CC samples (e.g., blood, urine, brain, prostate gland, placenta, testis
 CC and spleen) as diagnostic markers for conditions such as Alzheimer's
 CC disease, epilepsy, cancer, inflammation, infertility and prostatic
 CC hypertrophy. Sequences AAB11712 and AAB11714 represent human BSSP6
 CC variants (hbSSP6), and sequence AAB11713 represents murine BSSP6
 CC (mbSSP6).
 SO Sequence 275 AA:
 Query Match 98.2%; Score 1240.5; DB 21; Length 275;
 Best Local Similarity 90.2%; Pred. No. 3,4e-111;
 Matches 230; Conservative 0; Mismatches 0; Indels 25; Gaps 1;

QY 1 RIIGFECKPHSOPWQAALFEKTRLLCGATLLAPRWLLTAAHCLKP----- 46
 DB 21 RIIGFECKPHSOPWQAALFEKTRLLCGATLLAPRWLLTAAHCLKPWSITSPTHVSPDL 80
 QY 47 -----RYVHLCGHNLOKEGCEQRTATESPFPFGNNSLPKNDHRNDIMLVK 95
 DB 81 SSSNVCLSHSRYTVHLCGHNLOKEGCEQRTATESPFPFGNNSLPKNDHRNDIMLVK 140
 QY 96 MASPSITWAVRPLTSSRCVTAGTSCITSGSGSSSPQLRPHRLRCANITITIEHOKCE 155
 DB 141 MASPSITWAVRPLTSSRCVTAGTSCITSGSGSSSPQLRPHRLRCANITITIEHOKCE 200
 QY 156 NAYPGNITDTMWCASVOEGKRSQGDSPGPLVCNOSLOGIISMGODPCATITRRKPGVYTK 215
 DB 201 NAYPGNITDTMWCASVOEGKRSQGDSPGPLVCNOSLOGIISMGODPCATITRRKPGVYTK 260
 QY 216 VCKYVDWIOETMKN 230
 DB 261 VCKYVDWIOETMKN 275

RESULT 15
 AAB21312
 ID AAB21312 standard; Protein; 228 AA.
 AC AAB21312;
 DT 02-FEB-2001 (first entry)
 DE Human TLSP.
 DE XX
 KW Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6; TLSP;
 KW trypsin-like serine protease; kallikrein-like protein; serine protease;
 KW cytosolic; cancer; prostrate cancer.
 OS Homo sapiens.
 PN WO200053776-A2.

```

XX 14-SEP-2000
PD 09-MAR-2000; 2000MO-CA00258.
XX
XX 11-MAR-1999; 99US-0124260.
PR 01-APR-1999; 99US-0127386.
PR 21-JUL-1999; 99US-0144919.
XX
XX (MOUN ) MOUNT SINAI HOSPITAL.
XX
XX Yusef GM, Diamandis EP;
XX
XX WPI; 2000-587440/55.
XX
XX New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L
PT protein mediated disorders, especially cancer.
XX
XX Example 3; Fig 9; 184pp; English.
XX
XX The present sequence is human trypsin-like serine protease (TLSP), a
CC member of the kallikrein multi-gene family. Kallikreins and
CC kallikrein-like proteins are a subgroup of the serine protease enzyme
CC family. They catalyze the selective cleavage of specific polypeptide
CC precursors to release peptides with potent biological activity. Nucleic
CC acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4,
CC KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the
CC treatment, monitoring and diagnosis of cancers, especially prostate
CC cancer. They can also be used to identify a substance that can associate
CC with or mediate the biological activity of the proteins. Antibodies can
CC be used to treat conditions mediated by the kallikrein-like proteins.
XX
SQ Sequence 228 AA:
Query Match 97.9%; Score 1236; DB 21; Length 228;
Best Local Similarity 100.0%; Pred. No. 7.2e-111;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RITKGFECKPHSQPQNALFEKTRLLCGATLLPRLMTAHCCKPRYIVHGGHNLQKE 60
DB 4 RITKGFECKPHSQPQNALFEKTRLLCGATLLPRLMTAHCCKPRYIVHGGHNLQKE 63
QY 61 ECGEQTRTATESPFPFGFNNSLPNKDRNDIMLVKMASPVSTWAVRPLTLSSRCVTAGT 120
DB 64 ECGEQTRTATESPFPFGFNNSLPNKDRNDIMLVKMASPVSTWAVRPLTLSSRCVTAGT 123
QY 121 SCLISGSGSTSSPQLRLPHTLRCANITIIIEHOKCENAYPGNITDTWVCASVQEGKDSQ 180
DB 124 SCLISGSGSTSSPQLRLPHTLRCANITIIIEHOKCENAYPGNITDTWVCASVQEGKDSQ 183
QY 181 GDSGGLVNCNSLGGIISGODPCATTRKPGYTKVCKYVDWIOE 225
DB 184 GDSGGLVNCNSLGGIISGODPCATTRKPGYTKVCKYVDWIOE 228

```

Search completed: December 23, 2002, 14:19:06
Job time : 81 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 23, 2002, 14:21:47 ; Search time 2231 Seconds

(without alignments)
1669,638 Million cell updates/sec

Title: US-09-856-320a-2_COPY_53_282

Perfect score: 1263

Sequence: 1 RIITGFECKPHSOPMOMALF.....GVYTKCKYVDMIOETMKN 230

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xip
-O=/cgr2_1/USPTO.spool/US09856320/runat_23122002_113712_22707/app_query.fasta_1.391
-DB=EST -OPMT=fastap -SUFFIX=first -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US09856320.ccsn_1.1_2024_@runat_23122002_113712_22707 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMALP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-YARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YARNPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estdb:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estmuv:*
6: em_estov:*
7: em_estpl:*
8: em_estro:*
9: em_estl:*
10: qd_est2:*
11: qd_est3:*
12: qd_est4:*
13: qd_est5:*
14: qd_est6:*
15: em_estfun:*
16: em_estcom:*
17: qd_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	1228.5	97.3	1294	11 BC015551	BC015551 Homo sapi
2	1158	91.7	841	13 B1818697	B1818697 603037514
3	1146	90.7	678	13 B1763040	B1763040 603047836
4	1146	90.7	833	12 BG720793	BG720793 602692015
5	1117.5	88.5	1072	13 BM559782	BM559782 AGENCOURT
6	1067	84.5	1295	11 AK009360	AK009360 Mus muscu
7	1067	84.5	1295	11 AK009720	AK009720 Mus muscu
8	1066.5	84.4	1074	13 BM559617	BM559617 AGENCOURT
9	1041	82.4	1269	11 AK009659	AK009659 Mus muscu
10	963	76.2	708	12 BG697071	BG697071 602660281
11	857	67.9	639	12 BG747134	BG747134 602704354
12	793.5	62.8	973	12 BE867930	BE867930 601443517
13	780	61.8	761	14 BM982377	BM982377 UT-CE-EN1
14	724	57.3	467	9 A1893370	A1893370 mJ99h09.Y
15	720	57.0	467	9 AA073833	AA073833 mJ99h09.Y
16	669	53.0	539	14 BM837078	BM837078 K-EST0113
17	632	50.0	1048	11 AK004807	AK004807 Mus muscu
18	628.5	49.8	1240	11 AK003996	AK003996 Mus muscu
19	620.5	49.1	368	9 AA412318	AA412318 zB27C06.T
20	607	48.1	451	14 W60374	W60374 zD28B01.T1
21	605	47.9	754	13 B1653899	B1653899 603280742
22	599.5	47.5	890	11 AK009217	AK009217 Mus muscu
23	591	46.8	394	10 BE150851	BE150851 RC4-HT027
24	590	46.7	799	11 AK007843	AK007843 Mus muscu
25	589	46.6	799	11 AK008660	AK008660 Mus muscu
26	589	46.6	802	11 AK003064	AK003064 Mus muscu
27	587	46.6	802	11 AK003064	AK003064 Mus muscu
28	587	46.5	956	12 BF164946	BF164946 601778180
29	577	45.4	759	13 BJ502684	BJ502684 Mus muscu
30	573	45.4	815	11 AK003082	AK003082 Mus muscu
31	571.5	45.2	877	11 AK002278	AK002278 Mus muscu
32	567	44.9	904	13 B1759204	B1759204 603042631
33	567	44.9	1051	13 BM547198	BM547198 AGENCOURT
34	565.5	44.8	820	12 BG686173	BG686173 602787278
35	565	44.7	809	12 BF679282	BF679282 602153475
36	564.5	44.7	856	11 AK007406	AK007406 Mus muscu
37	562.5	44.5	759	9 A1326340	A1326340 m161e08.X
38	561.5	44.5	760	12 BF538381	BF538381 602053872
39	561.5	44.5	860	12 BG686885	BG686885 602784464
40	561	44.4	733	12 BG270402	BG270402 1b14903.Y
41	556.5	44.1	582	10 AM243944	AM243944 x091B07.X
42	556.5	44.1	808	13 BM438186	BM438186 IDLVR0020
43	556	44.0	734	12 BG270328	BG270328 1b13e05.Y
44	553.5	43.8	827	12 BG685835	BG685835 602788248
45	553	43.8	870	11 AK007773	AK007773 Mus muscu

ALIGNMENTS

RESULT 1
BC015551
LOCUS BC015551 1294 bp mRNA H7C 29-OCT-2001
DEFINITION Homo sapiens, kallikrein 11, clone IMAGE:3847565, mRNA.
ACCESSION BC015551
VERSION BC015551.1 GI:15930236
KEYWORDS H7C.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1294)
TITL Strausberg R.
JOURN Submitted (01-OCT-2001) National Institutes of Health, Mammalian


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DB: 13 Gaps: 0
US-09-856-320a-2_COPY_53_282 (1-230) x B1818697 (1-841)
QY 7 GUCUAYSPROHISSEGIN-PROTRPGNIAIALEUPHEGLUYSRHRARGLEU 26
DB 2 GAGGCGAAGCCTCACCTCCAGTCCGCGAGGCGCCCTCTGCGAAGAGCGCGCTACT 61
QY 26 UCYSGLYALATHRLEULEIAAPROARGTRPLEULEUTHRALAIAHISCYSEULYSPT 46
DB 62 CTGGGGGGCCACGCTATCCGCCAGATGCTCTCTACAGCAGCCCACTGCTCAAGCC 121
QY 46 OARGTYRILEVALHISLEUGLYGNHISASINLEUGINLYSGUINUGLYCYSGUINLTH 66
DB 122 CCCTATAGATTACCTGGGGGAGCACAACCTCCAGAGAGAGAGGGCTGTGAGCAGAC 181
QY 66 IARG-THRALATHRGLUSERPHEPROHISPROGLYPHEANANSEULEUPROASINLSA 86
DB 182 CCTGGACAGCCACTGAGTCTCTCCCAACCCCGGCTTCAACACAGCTCCCAACAAAG 241
QY 86 SPHISARGAASAPILMELEUVALYSMETALASERPROVALSER-IIEHTRTPALA 105
DB 242 ACCACCCCAATGACATATGCTGTGAAGATGGCATGCCAGTCTCTATCACCTGGGCT 301
QY 106 VALARGPROLEUTHRLEUSERSERARGCYSAIETHRALAGLYHRSERYSEULEI 125
DB 302 GTGGGACCCCTCACCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
QY 126 GLYTRPGLYSERTHRSESRERPROGLINLEUARGLEUPROHISRHRLEUARGCYSAIAASN 145
DB 362 GGGGGGGGACGAGTCCACCCCACTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
QY 146 IIEHTRILEIIEGLIHISGLINLYSCYSGLUASNAIATYRPROGLYASNIETHRASPTHR 165
DB 422 ATCACCATCTTGGAGCAGCAAGAGTGTGAGAGAGCCCTACCCGCAACATCACAGAAC 481
QY 166 METVALCYSAIASERVALGINLIU-GLYGLYLYSASPSERCYSGINLYSASERGILY 185
DB 482 ATGTGTGTCTCCAGCGTGCAGAGAGGGGCAAGAGACTCTCCGACAGGCTGACTCCGGGG 541
QY 185 YPROLEUVALCYASINLEUINSEULEGIN-GLYILEIIESETRPGLYGLNASPPTCYSA 205
DB 542 CCCTGCTGTGTGTAACAGTCTCTCAATGCAATATCTCTGGGGCAGAGATCCGCTG 601
QY 205 IAIETHRARGLYSPROGLYVALTYRTHRYSVALCYSLYSTYFVALASPTRPIL 225
DB 602 CGATACACCGCAAGCCGTGCTACACAGAAAGTCTGCAATATATGTGAGTGTGATCCAG 661
QY 225 IUTHRECTLYSASNASN 230
DB 662 AGACGATGAAGAACAT 678

RESULT 3
BI763040 678 bp mRNA 1linear EST 25-SEP-2001
LOCUS B1763040 603047836F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:518786 5',
DEFINITION mRNA sequence.
ACCESSION B1763040
VERSION B1763040.1 GI:15754618
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/
AUTHORS 1 (bases 1 to 678)
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLML1469 row: h column: 09
High quality sequence stop: 647.
Location/Qualifiers
1. 678
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:518786"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/Note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; site.1: NotI; site.2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

BASE COUNT 152 a 234 c 172 g 120 t
ORIGIN

Alignment Scores:
Pred. No.: 3 97e-112 Length: 678
Score: 1146.00 Matches: 210
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 1
Query Match: 90.74% Indels: 0
DB: 13 Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x B1763040 (1-678)
QY 20 PHEGLIULSYTHRARGLEULEUCYSGLYALATHRLEULEIAPROARGTRPLEULEUTHR 39
DB 10 TTGGAGAGAGGGGGCTACTCTGTGGGGCAGCCTATCCGCCCAATGCTGCTGAC 69
QY 40 AIAIAHISCYSEULYSPTOARGTYRILEVALHISLEUGLYGNHISASINLEUGINLYS 59
DB 70 GCAGCCACAGCTCAAGCCCGCTACATGACTCCTGCGGGAGCAGCAACCTCCAGAA 129
QY 60 GLUGLUGLYSGUINLTHRARGTRTHRALATHGLUSERPHEPROHISPROGLYPHEASN 79
DB 130 GAGGAGGGCTGTGAGCAGCCGAGCAGCCATGAGTCTTCCCAACCCCGGCTTCAAC 189
QY 80 ASINSEULEUPROASINLSAASPHISARGASNPILMELEUVALYSMETALASERPRO 99
DB 190 AACAGCCTCCCAACAAAGCAGCAGCAATGACATGATGCTGTGAGAGATGCCCA 249
QY 100 VALSERILEHTRTPALAVALARPROLEUTHRLEUSERSERARGCYSAIETHRALAGLY 119
DB 250 GTCTCATACCTCGGGCTGTGACACCCCTCTCCACAGCTGTGTACCTGCTGCTG 309
QY 120 THRSECYSEULEIIESERGLYTRPGLYSERTHRSESRERPROGLINLEUARGLEUPROHIS 139
DB 310 ACCAGCTGCTCATTTCTCCGCTGGGAGCAGCTCAAGCCCAAGTACGCTGCTCAC 369
QY 140 THRLEUARGCYSAIAASNILEHTRILEIIEGLIHISGLINLYSCYSGLUASNAIATYRPT 159
DB 370 ACCTTGGAGAGGCCCAACATCACATCATGAGACACAGAAAGTGAAGAGCTTACCC 429
QY 160 GLYASNIETHRSPHRMETVALCYSAIASERVALGINLIUGLYGLYASPSERCYS 179
DB 430 GGCACACATCACACACCAAGGTGTGCCAGCTCAGAAAGGGGGCAAGGACTCTCC 489
QY 180 GLNGLYASPSERCYGLYPTROLEUVALCYASAGINSEULEINGLYILEIIESETRP 199
DB 490 CAGGTGACTCCGGGGGCTCTGTGCTGTACCAAGTCTTCAAGGCAATTATCTCTGG 549

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QY 200 GYGLINAspProcysAlaIlethArGlySPROGLyValTyrThrIysValCysLysTyr 219
 DB 550 GGGCAGATCCGTCGTCGATCAAGCCGAGCTGGTGTACAGAAAGTCTGCAATAT 609
 QY 220 ValAspTPIleGlnGlnIurhMetLysAsnAsn 230
 DB 610 GTGGACTGGATCCAGAGACGATGAAGAACAT 642

RESULT 4
 BG720793 853 bp mRNA linear EST 08-MAY-2001
 LOCUS 602692015F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:4824387 5',
 DEFINITION mRNA sequence.
 ACCESSION BG720793
 VERSION BG720793.1 GI:13999980
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 1 (bases 1 to 853)
 NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shihaki
 Toshiyuki and Piero Carninci (RIKEN)
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 cDNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM10735 row: n column: 04
 High quality sequence stop: 826.

FEATURES
 Source
 1. 853
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4824387"
 /clone_11b="NIH_MGC_97"
 /lab_host="DH10B"
 /note="Organ: testis; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',
 size-selected for average insert size 2.2 kb and
 normalized for ROP 5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NHGRI, National
 Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 180 a 285 c 227 g 161 t
 ORIGIN

Alignment Scores:
 Pred. No.: 5.72e-112 Length: 853
 Score: 1146.00 Matches: 217
 Percent Similarity: 98.19% Conservative: 0
 Best Local Similarity: 98.19% Mismatches: 3
 Query Match: 90.74% Indels: 2
 DB: 12 Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x BG720793 (1-853)

QY 1 ArgIleIleLysGlyPheGlnLysProHisSerGlnProTglnAlaIleLeuPhe 20
 DB 193 AGGATCATCAAGGGGTTCAGATCAAGCTCCACGCTGGAGGACCCCTGTTC 252

QY 21 GlnTyrThrArgLeuLeuGlyAlaThrLeuIleAlaProArgTyrLeuThrAla 40
 DB 253 GAGAAAGACGGGCTACTCTGTGTGGGGGACGCTATCGCCCAAGATGGTCTCTGACAGCA 312

QY 41 AlaHisCysLeuLysProArGlyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
 DB 313 GGGCAGATCCGTCGTCGATCAAGCCGAGCTGGTGTACAGAAAGTCTGCAATAT 372

QY 61 GlnGlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 80
 DB 373 GAGGGGTGTGACAGACCCGAGACGCTGAGTCCCTCCAGCCCGGCTTCAACAAC 432

QY 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetLysSerProVal 100
 DB 433 AGCGTCCCAACAAAGACACACCGCATGACATCATCTGTGTGAAGATGGCATCGCCAGTC 492

QY 101 SerIleThrTyrPalayaIarProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
 DB 493 TCCATACCTGGGCTGTGTGACCCCTCACCTCTCTCTCAGCTGTGTACTGTGGCACCC 552

QY 121 SerCysLeuIleSerGlyrProGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
 DB 553 AGCTGCTCATTTTCGGGCTGGGGGACACGCTCCAGCCCGGCTTACGCTGCTCACACC 612

QY 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnLysAsnAlaTyrProGly 160
 DB 613 TTGGCATGGGCGCAACATCATCATTCATGACACAGAAAGTGTGAGAGACGCTACCCGGCG 672

QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
 DB 673 AACATCACAGACACCATGTGTGTGTCCAGCGTCGAGAAAGGGGCAAGACATCTGCGCAG 732

QY 181 GlyAspSerGlyGlyProLeuVal-CysAsnGlnSerLeuGlnGlyIleIleSerTrop1 200
 DB 733 TT-GACTCCGGGGGCCCTGTGTGTGTACCAAGTCTTCAAGGCAATATATCTCCGGGT 791

QY 200 yGlnAspProcysAlaIleThrArGlySPROGLyValTyrThrIysValCysLysTyr 220
 DB 792 GCAGATTCGTCGTGTCGATCAAGCCGAGCTGGTGTCTACAGAAAGTCTGCAATATCT 851

QY 220 1 220
 DB 852 G 852

RESULT 5
 BM559782 1072 bp mRNA linear EST 20-FEB-2002
 LOCUS BM559782
 DEFINITION AGENCOURT_6565460 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5744410
 5', mRNA sequence.
 ACCESSION BM559782
 VERSION BM559782.1 GI:18803655
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 1 (bases 1 to 1072)
 NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM12765 row: 1 column: 11
 High quality sequence stop: 684.

FEATURES
 Source
 1. 1072
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5744410"
 /clone_11b="NIH_MGC_119"

```

/tissue_type="medulla"
/lab_host="DH10B"
/Note="Organ: brain; Vector: PCMV-SPORT6; Site: 1: NotI;
Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH-MGC library."

```

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BASE COUNT      238 a      340 c      307 g      185 t      2 others
ORIGIN

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```

Alignment Scores:
Pred. No.:      9,14e-109      Length:      1072
Score:          1117.50      Matches:      213
Percent Similarity: 95.56%      Conservative: 2
Best Local Similarity: 94.67%      Mismatches: 7
Query Match:      88.48%      Indels:      3
DB:              13      Gaps:      1

```

```

US-09-856-320a-2_COPY_53_282 (1-230) x BM559782 (1-1072)

```

```

QY 1 Argillelelysglypheglucyslyspromisserglnprotrpglnalalauphe 20
    |||||||
DB 272 AGGATCATCAAGGGGCTCGAGTGCACGCCCTCCAGCCCTCGCAGGAGCCCTGTC 331
    |||||||
QY 21 GlulysThrargyleuleucysglyAlaThrleuileAlaProargtrpleuThrAla 40
    |||||||
DB 332 GAGAAAGACGGGGCTACTCTGGGGGCGACGCTCATGCCCCCAATAGTGGCTTGACAGCA 391
    |||||||
QY 41 AlahiscysleuysProargTyrlleValhislenglylnhlsasnleuglnlyslu 60
    |||||||
DB 392 GCCACAGCTCCCAAGCCCGCTCATAGTTCACCTGGGGGAGCAGCAACCTCCAGAGAG 451
    |||||||
QY 61 GlulyscysgluglnThrargThrAlaThrGluSerPheProhlsProglyPheAsn 80
    |||||||
DB 452 GAGGGCTGTAGCAGACCCCGACAGCCACGACGCTTCCGCCACCCGCTTCAACAC 511
    |||||||
QY 81 SerleuproasnlyspasphlsarpsasnplleuMetleuVallysmetAlaserProval 100
    |||||||
DB 512 AGCCTCCCAAGACACCGACATGATCATCTGCTGTAAGATGAGATGCCAGTC 571
    |||||||
QY 101 SerleuThrAlaValaArgProleuThrleuSerSerargCysValaThrAlaGlyThr 120
    |||||||
DB 572 TCCATACCTCGNGCTGGCAGACCCCTCACCCTCCACGCTGTCTCAGCTGGCAGCC 631
    |||||||
QY 121 SerCysleuileserglyTrpglySerThrSerSerProglInleuArgleuProhlsThr 140
    |||||||
DB 632 AGCGGCTCATTTCCGGCTGGGGGAGACGCTCCAGCCCGCAGTTACGCTGCCACACC 691
    |||||||
QY 141 LeuArgysAlaasnleuThrlelleleGlnhlsGlnlyscysGluAsnAlaTyrrProgly 160
    |||||||
DB 692 TTGGGATGGCCCAACATCCATCATTCATGACACACAGAAAGTGTGAAGCGCTTACCCCGG 751
    |||||||
QY 161 AsnleuThrAspThrmetValcysAlaSerValGlnGlnlygllyAspSerCysGln 180
    |||||||
DB 752 CACATCAACACACACATGCTGTGGCCAGCGTGCAGAGAGGGGCGACAGCATCTCGCNCA 811
    |||||||
QY 181 GlyAspSerlygllyProleuValcysAsnGlnSerleuGlnlylleleSerTrpgly 200
    |||||||
DB 812 GGGGACGCCGGGGGCGCTCGTGTGTGAACAGCTCTTCAAGGCAATATCTCGGGGC 871
    |||||||
QY 201 -GlnAspProCysAlaAlaThrarglyspProglyValTyrrThr---tylValCyslysty 219
    |||||||
DB 872 CCAAGATCCGCTGTGCGATCACCGGAAAGCCTGCTGTACCGGAAAGGCTTGCACATA 931
    |||||||
QY 219 rVal-AspTrp 222
    |||||
DB 932 TGTGGGACTGG 942

```

RESULT 6

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AK009360
LOCUS      1295 bp      mRNA      linear      HTC 19-JAN-2002
DEFINITION Mus musculus adult male tongue cDNA, RIKEN full-length enriched
            library, clone:2310015108:protease, serine, 20, full insert
            sequence.
ACCESSION  AK009360
VERSION    AK009360.1 GI:12844110
KEYWORDS   HTC; CAP trapper.
SOURCE     Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA,
            clone:2310015108.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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REFERENCE
AUTHORS   Carninci,P. and Hayashizaki,Y.
TITLE     High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
MEDLINE   99279253
PUBMED    10349636

```

```

REFERENCE
AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE   20499374
PUBMED    11042159

```

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REFERENCE
AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsuana,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wachihi,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.
TITLE     RIKEN integrated sequence analysis (RISA) system -384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE   20530913
PUBMED    11076861

```

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REFERENCE
AUTHORS   Kawai,J., Shingawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamana,I.,
            Saito,T., Okazaki,Y., Gojohori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staudli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustlincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzerelli,J., Mombærts,P., Nordone,P.,
            Ring,B., Rindwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-Oka,K., Wang,K.H., Weitz,C., Whitaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohsaki,S.,
            and Hayashizaki,Y.
TITLE     Functional annotation of a full-length mouse cDNA collection
JOURNAL   Nature 409 (6821), 685-690 (2001)
MEDLINE   21085660
PUBMED    11217851

```

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REFERENCE
AUTHORS   5 (bases 1 to 1295)
            Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Haneagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiroaka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,

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US-09-856-320A-2_COPY_53_282 (1-230) x AK009360 (1-1295)

QY	1	Arg1leileuylgylpheglnucysylprohisserginprotpglnalaaleu	20
Db	282	AGGATCATCAAGGTTATATAGTCAGAGGCTCTACTACAGCCATTGCGAGTGGCCCTTT	341
QY	21	GlulysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTPLeuLeuThra	40
Db	342	CAGAAACACAGCGTTCTGTGGGCAACCCCTCATCGCCCCCAATAGGCTCTGACAGCA	401
QY	41	AlaHisCysLeuLeuYerProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu	60
Db	402	GCCCACTGGCCGCAAGCCCATTTACGTGATGATCCCTTGGAGAGACAAATCTAGAACAAACA	461
QY	61	GlulGlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyIlePheAsn	80
Db	462	GAGCGCTGTGACAGAGGCGGATGCGCACTAGTCTCTCCCAACCCCGACTTACAAAC	521
QY	81	SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal	100
Db	522	AGCCTCCCAACAAAGACCAACCGGAATGACATTAATGCTTGGAGAGATGTGTCGCCGTC	581
QY	101	SerIleThrThrAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr	120
Db	582	TTCTTACCCGAGCTGTGACGACATCCACTGCTCCCACTGTGTGTGCGCAGCGACC	641
QY	121	SerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThr	140
Db	642	AGCTGCTCATTTCTTGATGGGAGCAACAGTCACACCCCAAGTTGGCGCTCTCATATCC	701
QY	141	LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGly	160
Db	702	TTTCGATGTGCCAATGTCTCCATCTCAACACAAAGAGTGTCGAAGAGCGCTTACCCGGCG	761
QY	161	AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln	180
Db	762	AACATGACAGACACCAATGCTGTGCCAGTCTTCGAAAGAGGGCAAGAGACTCTGTGAC	821
QY	181	GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGly	200
Db	822	GGGACATCTGGAGAGGCCCTCGTGTCTGCAACGAGATCTCTCAAGGCATCATCTCTGGGGT	881
QY	201	GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal	220
Db	882	CAGAGCCCATGTGCGCTCACAGAAAGCCTGTGTCATACAAAAGTCGCAATACTTT	941
QY	221	AspTrrIleGlnGluThrMetLysAsnAsn	230
Db	942	AACGTGATCCACGAGGTATGAGAACAAAT	971
RESULT 7			
LOCUS	AK009720		
DEFINITION		Mus musculus adult male tongue cDNA, RIKEN full-length inserted library, clone:2310040F07;protease, serine, 20, full insert sequence.	
ACCESSION	AK009720		
VERSION	AK009720.1		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (strain: C57BL/6J) adult male tongue cDNA to mRNA, clone:libRIKEN full-length enriched mouse cDNA library		
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			

Db 642 AGTCGCTCATTTTCGATGGGGACACAGTCACAGCCCGCTGCTCATTC 701
 Qy 141 LeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGly 160
 Db 702 TTGCGATGTGGCCATGTCTCATTCAGAACACAGAGAGTGTGAGAGGCGCTACCGCGGG 761
 Qy 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
 Db 762 AACATCACAGACACCAATGCTGGCCAGCTGTCGGAAGAGGCAAGACATCTCTGTGAG 821
 Qy 181 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTProGly 200
 Db 822 GGGATCTGGAGAGCCCGCTGGCTGCAACGATCTCTTCAGAGCATCTCTCTGGGT 881
 Qy 201 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysIleTyrVal 220
 Db 882 CAGGACCCATGTGGCCGTCCACAGAAAGCCTGGGTCTATACAAAGTGTGCAATACTTT 941
 Qy 221 AspTrrIleGlnGluThrMetLysAsnAsn 230
 Db 942 AACTGATCCACGAGGTATGAGGAACAAT 971

RESULT 8
 BM559617 1074 bp mRNA linear EST 20-FEB-2002
 LOCUS AGENCOURT.6565456 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5744314
 DEFINITION 5', mRNA sequence.
 ACCESSION BM559617
 VERSION BM559617.1 GI:18803348
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 1074)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-riemail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM12765 row: h column: 11
 High quality sequence stop: 689.

FEATURES
 Source Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:5744314"
 /clone_lib="NIH_MGC_119"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: Not;
 site: 2: EcorV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcorV site is destroyed upon
 cloning). Average insert size 1.3 kb. Insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH MGC Library."

BASE COUNT 238 a 339 c 311 g 184 t 2 others
 ORIGIN

Alignment Scores: 2.59e-103 Length: 1074
 Pred. No.: 1066.50 Matches: 213
 Percent Similarity: 92.318 Conservative: 3

Best Local Similarity: 91.03% Mismatches: 12
 Query Match: 84.44% Indels: 6
 DB: 13 Gaps: 1
 US-09-856-320a-2_copy_53_282 (1-230) x BM559617 (1-1074)

Qy 1 ArgIleIleLysGlyPheGluCysLysProHisSerGlnProTrrGlnAlaLeuPhe 20
 Db 271 AGGATCATCAAGGGGCTTCCAGATGCAAGCCTCATCTCCACCGCTGGACAGACCCCTGTC 330
 Qy 21 GlnLysThrArgLeuLeuGlyGlyAlaThrIleIleAlaProArgTrrLeuThrAla 40
 Db 331 GAGAAAGCCGGCTACTGTGTGGGGAGAGCTCATGCCCCCAGATGGCTCTGTACAGCA 390
 Qy 41 AlaHisCysLeuLysProArgTrrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
 Db 391 GCCCATGCTCTCAAGCCCGCGTACATAGTTCACCTGGGGACACACACTCCAGAAAGAG 450
 Qy 61 GlnGlyCysGlnGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsn 80
 Db 451 GAGGCGTGTGACAGACAGCCGAGACAGCAGTGAAGTCTTCCCGCCACCGCTTCAACAC 510
 Qy 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
 Db 511 AGCTTCTCCCAACAAAGACACCGCAATGATCATCTGTGTGAAGATGGCATCGGCAGTC 570
 Qy 101 SerIleThrTrrPAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
 Db 571 TCCATCATCTGGGGCTGTGTGGAGCCCTCACCCCTCTCTCACGCTGTCTCCTGTGGCACC 630
 Qy 121 SerCysLeuIleSerGlyTrrPglySerThrSerProGlnLeuArgLeuProHisThr 140
 Db 631 ACCTGCTCATTTCCGGGCTGGGGAGACAGCATCGACAGCCCGCTACAGCTGCTCATCAC 690
 Qy 141 LeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGly 160
 Db 691 TTGCGATGTGGCCATGTCTCATTCAGAACACAGAGTGTGAGAGGCGCTACCGCGGG 750
 Qy 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
 Db 751 CACATCACAGACACCATGTGTGTGTGTCACAGCCTGCAGAGAGGGCGACATCTCTGNCAG 810
 Qy 181 GlyAspSer-GlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrrP-G 200
 Db 811 GGTGACTCGGGGGGGCCCTGT 870
 Qy 200 LysGlnAspProCys-AlaIleThrArgLys-ProGlyValTyrThrLysValCysLysTyr 219
 Db 871 GGCAGNATCCGTGTGCGATCACCCGAAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 930
 Qy 219 rVal--AspTrrIle-GlnGluThrMetLys 228
 Db 931 AATGTGGGAGCTGTGATCCCGGAGACCATGTGAG 962
 RESULT 9
 AK009659 1269 bp mRNA linear HTC 19-JAN-2002
 LOCUS AK009659 Mus musculus adult male tongue cDNA, RIKEN full-length enriched
 DEFINITION library, clone:2310037E23:protease, serine, 20, full insert
 sequence.
 ACCESSION AK009659
 VERSION AK009659.1 GI:12844589
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA,
 clone_lib:RIKEN full-length enriched mouse cDNA library
 clone:2310037E23.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)

MEDLINE
 PUBMED
 99279253
 10349636
 REFERENCE
 AUTHORS
 2
 Carrinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE
 PUBMED
 10499374
 11042159
 REFERENCE
 AUTHORS
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carrinci, P.,
 Suni, H., Akiyama, J., Nishik, K., Kitunai, T., Tashiro, H., Itoh, M.,
 Konno, H., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaiguchi, S., Ikegami, T., Kasaiwagi, K.,
 Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE
 PUBMED
 20530913
 11076861
 REFERENCE
 AUTHORS
 4
 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
 Aizawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,
 Salto, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Salto, R.,
 Kadote, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
 Fleischmann, Y., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
 Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, T., Pesole, G.,
 Quackenbush, J., Schmitt, L. M., Staib, F., Suzuki, R., Tomita, M.,
 Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
 Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
 Carrinci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
 Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
 Hofmann, M., Hume, D. A., Kamaly, M., Lee, N. H., Lyons, P.,
 Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
 Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
 Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storch, K. F., Suzuki, H.,
 Toyok, O., K., Wang, K. H., Weitz, C., Willeker, C., Wilming, L.,
 Wyszynski, B., A., Yoshida, K., Hasegawa, Y., Kawai, J., Kotsuki, S.,
 and Hayashizaki, Y.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)
 MEDLINE
 PUBMED
 21085660
 11217851
 REFERENCE
 AUTHORS
 5 (bases 1 to 1269)
 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,
 Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,
 Carrinci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hangaki, T.,
 Hara, A., Hayatsu, N., Hill, D., Yamamoto, K., Hiraoka, T., Hori, F.,
 Hume, D., Imoto, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T.,
 Kato, H., Kawai, J., Kojima, Y., Konno, H., Konda, M., Koya, S.,
 Kunita, C., Matsuyama, T., Miyazaki, A., Nishik, K., Nomura, K.,
 Numata, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,
 Salto, H., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
 Schmitt, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
 Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamana, I.,
 Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and
 Hayashizaki, Y.
 Direct Submission
 Physiol. (10-JUL-2000) Yoshihide Hayashizaki. The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Shuto-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
 URL: http://genome-gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 Please visit our web site (http://genome-gsc.riken.go.jp/) for
 further details.
 cDNA library was prepared and sequenced in Mouse Genome

FEATURES		Location/Qualifiers	
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		/organism="Mus musculus"	
		/strain="C57BL/6J"	
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		/db_xref="MGI:1894042"	
		/db_xref="taxon:10090"	
		/clone="2310037E23"	
		/sex="male"	
		/tissue_type="tongue"	
		/clone_lib="RIKEN full-length enriched mouse cDNA library"	
		/dev_stage="adult"	
		1..1269	
		/note="data source:MGI, source key:MGI:1929977, evidence:ISS	
		protease:.serine, 20"	
		/db_xref="MGI:1929977"	
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ORIGIN			
Alignment Scores:			
Score: No.:	1.79e-100	Length:	1269
Percent Similarity:	1041.00	Matches:	186
Best Local Similarity:	91.30%	Conservative:	24
Query Match:	80.87%	Mismatches:	20
DB:	82.42%	Indels:	1
	11	Gaps:	0
US-09-856-320A-2_COPY_53_282 (1-230) x AK009659 (1-1269)			
QY	1	Argllelleuysgclpheglucyalsyprohissersglnprotprglnalaleu	phe 20
Db	257	AGGATCATCAAGGGTTATGATGATGAGGCGTCACACAGCATGGAGGGCGCTCTTT	316
QY	21	GluGlyThrArgLeuLeuCySGlyAlaThrIleuIleAlaProArgTrpLeuThrAla	40
Db	317	CAGAAAGACACGCGTTCCTGTGGGGCAACCTCATCCGCCCCCAAAATGGCTTCGACAGCA	376
QY	41	AlaHisCysLeuIlyProArgTyrIleValHisIleuIlyGlnHisAsnIleuGlnIlyGlu	60
Db	377	GCCCACTGCGCCGAAGCCCATACGTATCTCTTGTGAAGGCAACAATCTAGAGAACACA	436
QY	61	GluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn	80
Db	437	GAGCGCTGTAGCGAGG-CGATGGCCACATGAGTCTTCCGCCACCCGACTTCACACAC	495
QY	81	SerLeuProAsnIlyAspHisArgAsnAspIleMetLeuValIlyMetAlaSerProVal	100
Db	496	AGCCTCCCAACAAGACACACCGGAATAGATATATGCTTGGAAAGATGTGCTCCGTC	555
QY	101	SerIleThrTrpAlaValArgProLeuThrIleuSerSerArgCysValThrAlaGlyThr	120
Db	556	TTCTTTTACCGAGGTGGACGCCACTACCCCTGTGCCACACATGTGTGCGTCGAGGCACC	615
QY	121	SerCysLeuIleSerGlyTyrPglYSerThrSerSerProGlnIleuArgLeuProHisThr	140
Db	616	AGCTGCTCATTTTGTGATGGGACACACATCCAGCCCAAGTTGGCGCTTCCTCATTC	675
QY	141	LeuArgCysAlaAsnIleThrIleIleGlnHisGlnIlyCysGluAsnAlaTyrProGly	160

Db 676 TTCGATGTCCTCATGTCCTCATGCAACACAGAGCTGTGAGAGCCCTACCCGGCC 735
 Qy 161 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGln 180
 Db 736 AACATCACAGACACATGCTGCGCCAGTGTTCGGAAAGAGGCAAGGACTCTGTGCAG 795
 Qy 181 GlyAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 200
 Db 796 GGTGACTCTGGAGAGCCCGCTGCTGCACAGGATCTCTTCAGGACATCATCTCTGGGGT 855
 Qy 201 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 220
 Db 856 CAGAGCCCATGTCCTCCCTCACACAGAAAGCTGTGTCTATACAAAGTCTGCAATACTTT 915
 Qy 221 AspTrpIleGlnGluThrMetLysAsnAsn 230
 Db 916 AACTGATCCAGAGGTATAGAGAACAT 945

RESULT 10
 LOCUS BG697071 708 bp mRNA linear EST 07-MAY-2001
 DEFINITION 602660281F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:480356 5',
 mRNA sequence.
 ACCESSION BG697071
 VERSION BG697071.1 GI:13962880
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
 TITLE NIH-MGC http://mgc.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-riemail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
 Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM10699 row: a column: 21
 High quality sequence stop: 704.

FEATURES
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 1..708
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:480356"
 /clone_lib="NCI_CGAP_Skn3"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site:1: NCI;
 Site:2: Sall; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 147 a 262 c 183 g 116 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.54e-92 Length: 708
 Score: 963.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 76.25% Indels: 0
 DB: 12 Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x BG697071 (1-708)

Qy 1 ArgIleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaIleLeuPhe 20
 Db 175 AGAGATCATCAAGGGGTTCAGATGCAAGCTCTACCTCCAGACCTGTGCGAGGAGCCCTGTTCC 234

Qy 21 GlnLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 40
 Db 235 GAGAAACGGGGCTACTGTGTGGGGAGCGCATCATGCCGCCAGATGGCTCTGACAGCA 294
 Qy 41 AlaHisCysLeuLysProArgTrpTrpIleValHisLeuGlyGlnHisAsnLeuGlnGly 60
 Db 295 GCCACTGGCTCAAGCCCGCTACATAGTTCACCTGGGAGACAGCAACCTCCAGAGGAG 354
 Qy 61 GlnGlyCysGlnGlnThrArgThrAlaThrGlnLysPheProHisProGlyPheAsn 80
 Db 355 GAGGGGTGGAGAGACCGCGAGAGCAGCTAGACTCTTCCCGCCCGGCTTCAACAC 414
 Qy 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
 Db 415 AGCCTCCCAACAAAGACCCGCAATGATCATGCTGTGTGATGATGATGATGATGATGAT 474
 Qy 101 SerIleThrAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
 Db 475 TCCATACCTGGGCTGTGGACCCCTCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 534
 Qy 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
 Db 535 AGTGCTCATTTCCGGCTGGGGGAGAGAGCTCCAGCCCAATGATGATGATGATGATGATGAT 594
 Qy 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGly 160
 Db 595 TTGCGATGCGCCACATCATCATCATGATGAGACAGAGAAAGTGTAGAAACCTTACCCGGC 654
 Qy 161 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAsp 177
 Db 655 AACATCACAGACACATGCTGTGTGCGAGCTGACAGAGAGGGGCGCAAGGAC 705

RESULT 11
 LOCUS BG747134 639 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602704354F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4857733 5',
 mRNA sequence.
 ACCESSION BG747134
 VERSION BG747134.1 GI:14057787
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE NIH-MGC http://mgc.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-riemail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM1710 row: k column: 14
 High quality sequence stop: 638.

FEATURES
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 /tissue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: colon; Vector: pORF7; Site:1: XhoI; Site:2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of

DEFINITION UI-CF-EN1-acs-o-17-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
 UI-CF-EN1-acs-o-17-0-UI 3', mRNA sequence.
 ACCESSION BM982377
 VERSION BM982377.1 GI:19605813
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 761)
 AUTHORS Bonaldi,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 9704447
 COMMENT Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
 The following repetitive elements were found in this cDNA sequence: 17-100, >LINE2 (matched complement)
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES
 source
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-CF-EN1-acs-o-17-0-UI"
 /clone_1lb="UI-CF-EN1"
 /tissue_type="Primary Lung Cystic Fibrosis Epithelial Cells"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-EN1 is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT.
 TAG_LIB=UI-CF-EN1
 TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h
 TAG_SEQ=CTGCTCAGGT"
 BASE COUNT 172 a 170 c 222 g 195 t 2 others
 ORIGIN

Alignment Scores:
 Pred. No.: 6.25e-73 Length: 761
 Score: 780.00 Matches: 143
 Percent Similarity: 99.318 Conservative: 0
 Best Local Similarity: 99.318 Mismatches: 1
 Query Match: 61.768 Indels: 0
 DB: 14 Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x BM982377 (1-761)

QY 87 HisArgAsnApIleUetUeUaUlyMetAlaSerProValSerIleThrTrpAlaVal 106
 |||||
 Db 761 CACCGCATGATCATCATGCTGTGMAAGATGATGCATCCGACATCTCCACCTGGCTGTG 702
 QY 107 ArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGly 126
 |||||
 Db 701 CGACCCCTCACCTCTCTCTACGATGTGTCATGCTGGCAGCCAGCTCCATTTCCGGC 642
 QY 127 TrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIle 146
 |||||
 Db 641 TGGGGCAGCAGCAGTCCAGCCGCCAGTTAGCGCTGCTCACACCTGGGATCGCCACATC 502
 QY 147 ThrIleIleGlnHisGlnCysGluAsnAlaTyrProGlyAsnIleThrAspThrMet 166
 |||||
 Db 581 ACCATCATTTGAGCAGCAGAAAGTGTGAGAGCGCTACCCGCAACATCACAGACCATG 522
 QY 167 ValCysAlaSerValGlnGlnGlyGlyValAspSerCysGlnGlnLysPserGlyPro 186
 |||||
 Db 521 GTGTGTCCAGCCTGTGAGGAAGGGGCAAGAGCTCTGTCAGGTACTCCGGGGCCCT 462
 QY 187 LeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIle 206
 |||||
 Db 461 CTGTGTCTGATCAGCATCTCTTCAAGCATTTATCTCTGGGCGCAGATCCGTGGCATC 402
 QY 207 ThrArgLysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnIle 226
 |||||
 Db 401 ACCGGAAGCGCTGTGTCTACGAAAGTCTGCAAAATATGTGACTGATTCAGGAGAGC 342
 QY 227 MetLysAsnAsn 230
 |||||
 Db 341 ATGAGAAACAT 330

RESULT 14
 A1893370 467 bp mRNA linear EST 15-MAR-2000
 A1893370
 LOCUS m199h09.y1 Soares mouse p3MwF19.5 Mus musculus cDNA clone
 DEFINITION IMAGE:484289.5, similar to gb:030785 Mouse mRNA for neuropsin, cds
 (MOUSE);, mRNA sequence.
 A1893370
 ACCESSION A1893370.1 GI:5599272
 VERSION
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 467)
 AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,T., Person,
 B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter,
 E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.
 TITLE The WashU-NCI Mouse EST Project 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LBNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 This read is a RESEQUENCE of a previously sequenced mouse clone
 This read has been verified (found to hit its original self in the
 correct orientation)
 Putative full length read
 vector to vector length is 833
 MG1:295033
 Seq primer: -40RP from Gibco
 High quality sequence stop: 445.
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 1..467
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 /db_xref="taxon:10090"

	/clone="IMAGE:484289"
	/dev_stage="19.5 dpc total fetus"
	/lab_host="DH10B (ampicillin resistant)"
	/note="Vector: pT73D (Pharmacia) with a modified
	polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
	was primed with a Not I - oligo(dN) primer [5',
	TGTTACCAATCTGAAGTCGGAGCGGCCCATTTTTTTTTTTTTTTT 3'] ,
	double-stranded cDNA was size selected, ligated to Eco RI
	adapters (Pharmacia), digested with Not I and cloned into
	the Not I and Eco RI sites of a modified pT73 vector
	(Pharmacia). Library went through one round of
	normalization to a Cot = 5. Library constructed by Bento
	Soares and M.Patima Bonaldo. RNA was kindly provided by
	Dr. Minoru Ko (Wayne State University)."
BASE COUNT	101 a 153 c 115 g 98 t
ORIGIN	
Alignment Scores:	
Pred. No.:	2.78e-67 Length: 467
Score:	724.00 Matches: 130
Percent Similarity:	91.61% Conservative: 12
Best Local Similarity:	83.87% Mismatches: 13
Query Match:	57.32% Indels: 0
DB:	Gaps: 0
US-09-856-320A-2_COPY_53_282 (1-230) x A1893370 (1-467)	
OY	63 CysgluGlntHrArgThAlarhrgluseRheProHisProglyPheasnaSertleu 82
Db	
	3 TGTGACGACGAGCCGATGCGCCTACTAGTCCTTCCCCACCCGACTTCAACAACAGCCCTC 62
OY	83 ProenLysAspHisARgsnAspileMetleuVallysMelaIaseProvalserile 102
Db	63 CCCAACAAAGACCACCGGATGACATAATGCTTGGAAGATGCTGCCTCCGCTCTCTT 122
OY	103 ThrTPAlaIalargProleuthrLeuserserArgCysValThrAlaglyThsercys 122
Db	:::::
OY	123 ACCCGAGCTGTGCACCACTCACCTGTGCCACACTGTGCGTCGACGAGCAGCCAGTCGC 182
OY	123 leuileSer glyTirgylSerthrSerserProginleuArgleuProHisthrleuArg 142
Db	183 CTCATTCTTGGATGGGGGACACGTCACGCCCCCGAGTGGCGCTGCCTCATTTCCITGGCA 242
OY	143 CysAlaasnlierThrIlellegluHISgluLysCysgluASnAlaTyProglysnlie 162
Db	243 TGTGCAATGTCTCATATATGACACAAAGAAGGTGTGAAGAGCCTACCGGGCAACATC 302
OY	163 ThrAspTrMetValCysAlaserValIngluglyLylyAspSerCysInglyasp 182
Db	303 ACAGACACCANTCTGTGGCCAGTGTGGAAAAGAGGCAAGACTCCTGTACAGGGTGAC 362
OY	183 SerGlyglProleuValCysasnleInsleuInglylleleSertPrglylnasp 202
Db	363 TGTGGAGGCCCCCTGTGTGCACAGCATCTCTTCAAGGCATCATCTCTGTGGGTCATGAC 422
OY	203 ProCysAlaIleThrArgLysProglyValTYrrhrLysValcys 217
Db	423 CCATGTGGCGTCACCAAGAAAGCTGTGTCTATACAAAAAGTCTGC 467
RESULT 15	
LOCUS	AA073833
DEFINITION	AA073833 467 bp mRNA linear EST 04-OCT-1996 mj99h09.1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:484289.5 similar to gb:U36092_rna4 TRYSINOMEN II PRECURSOR (HUMAN); gb:D30785 Mouse mRNA for neuropsin, cds (MOUSE);, mRNA sequence.
ACCESSION	AA073833
VERSION	AA073833.1 GI:1595581
KEYWORDS	EST.
SOURCE	house mouse,
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 467)	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
	Marrá,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,R., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.	The WashU-HHMI Mouse EST Project	Unpublished (1996)	Contact: Marrá M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MG1:295033 Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 322.
FEATURES	source	Location/Qualifiers		
	1..467	/organism="Mus musculus"		
	/db_xref="taxon:10090"			
	/clone_image="484289"			
	/clone_id="Soares mouse p33M919.5"			
	/dev_stage="19.5 dpc total fetus"			
	/lab_host="DH10B (ampicillin resistant)"			
	/note="Vector: pUT73D (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5], TGTTGACATCTGTAAGTGGAGGAGCGCCGATTTTTTTTTTTT 3', double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pUT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Patima Bonaldi. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."			
BASE COUNT	102 a	154 c	114 g	97 t
ORIGIN				
Alignment Scores:				
Pred. No.:	7,44e-67	Length:	467	
Score:	720.00	Matches:	130	
Percent Similarity:	91.61%	Conservative:	12	
Best Local Similarity:	83.87%	Mismatches:	13	
Query Match:	57.01%	Indels:	0	
DB:	9	Gaps:	0	
US-09-856-320A-2_COPY_53_282 (1-230) x AA073833 (1-467)				
QY	63 CysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeu	82		
DB	3 TGTGAGCAGAGCGATGGCCACCTGAGTCTTCCGCCACCCGAGCTTCAACAACAGCCTC	62		
QY	83 ProAsnLysASPHisArgAsnAspLleMetLeuValLysMetAlaSerProValSerIle	102		
DB	63 CCCAACAAAGACACCCGGATGATACATTAAGCTTGGAGATGTCGTCGCCCTCTCTTT	122		
QY	103 ThrTPAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyPheSerCys	122		
DB	123 ACCGAGAGCTGTGCAGACCACTACCTGTGCCACACTGTGTGGTCGACGACCAAGCTGC	182		
QY	123 LeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeuArg	142		
DB	183 CTCATTTCTGTGATGGGAGCACACGTCACGCCGCCAGTGGCGCTCCATTCCTTGGCA	242		
QY	143 CysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIle	162		
DB	243 TGTGCAATGTCATCATCGAACAACAGGAGTGTGAGAAGGCGCTTACCGGGCAACATC	302		

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 13:16:17 ; Search time 92 Seconds

(without alignments)
515.118 Million cell updates/sec

Title: US-09-856-320a-2_COPY_53_282

Perfect score: 1263
Sequence: 1 RIIKGFECRHSQPMQALF.....GVYTKVCKYVDWIQETMKNN 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1067	84.5	249	11 090YN4	09qyn4 mus musculus
2	1067	84.5	276	11 090YN3	09qyn3 mus musculus
3	681	53.9	255	4 096R00	096r00 homo sapien
4	632	50.0	251	11 09DBQ8	09dbq8 mus musculus
5	628.5	49.8	293	11 09D140	09d140 mus musculus
6	599.5	47.5	234	11 09CV76	09cv76 mus musculus
7	592	46.9	246	11 09ZIR9	09zir9 mus musculus
8	590	46.7	246	11 09QUK9	09quk9 mus musculus
9	589	46.6	246	11 09R0T7	09r0t7 mus musculus
10	588.5	46.6	239	11 063275	063275 rattus norv
11	587.5	46.5	235	11 063274	063274 rattus norv
12	586.5	46.4	261	11 09JW70	09jw70 mus musculus
13	579.5	45.9	261	6 09N1Q1	09n1q1 saginus oe
14	579.5	45.9	261	6 029474	029474 canis fami
15	565	44.8	251	11 054854	054854 rattus norv
16	565	44.7	249	11 091VE3	091ve3 mus musculus

17	564.5	44.7	247	11 09CPN7	09cpn7 mus musculus
18	563	44.6	262	4 08TCV8	08tcv8 homo sapien
19	562.5	44.5	237	13 091515	091515 fugu rubrip
20	562.5	44.5	244	13 08QGW3	08qgw3 anguilla ja
21	561.5	44.5	263	11 09JW71	09jw71 mus musculus
22	559.5	44.3	263	11 09JW69	09jw69 mus musculus
23	558.5	44.2	245	13 042160	042160 petromyzon
24	558	44.2	240	13 098TH0	098th0 engraulis j
25	558	44.2	246	11 088301	088301 mus musculus
26	558	44.2	253	11 091Y82	091y82 mus musculus
27	553	43.8	247	11 09CPN9	09cpn9 mus musculus
28	552.5	43.7	244	13 042159	042159 petromyzon
29	552.5	43.7	254	6 09XSN6	09xsn6 sus scrofa
30	551	43.6	238	13 09W706	09w706 paracichthy
31	549.5	43.5	247	13 042158	042158 petromyzon
32	548.5	43.4	247	13 042608	042608 petromyzon
33	548.5	43.4	261	11 088309	088309 mus musculus
34	547	43.3	247	11 09D7Y7	09d7y7 mus musculus
35	546.5	43.3	242	13 092099	092099 paracichthy
36	543.5	43.0	242	13 09W707	09w707 paracichthy
37	541.5	42.9	242	13 093266	093266 pseudopleur
38	540	42.8	241	13 098RG9	098rg9 engraulis j
39	540	42.8	247	13 09W705	09w705 paracichthy
40	532.5	42.2	249	13 09W6K0	09w6k0 notothenia
41	526.5	41.7	675	13 09W6J8	09w6j8 dissostichu
42	525.5	41.6	255	11 09JIS2	09jis2 mus musculus
43	519.5	41.1	249	13 092046	092046 dissostichu
44	519.5	41.1	255	11 0920M1	0920m1 mus musculus
45	503.5	39.9	344	13 09W6J9	09w6j9 dissostichu

ALIGNMENTS

RESULT 1

ID 090YN4 PRELIMINARY; PRT: 249 AA.
AC 090YN4;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAY-2002 (TREMblrel. 20, Last annotation update)
DE HIPPOSTASIN (2310015108RIK protein).
GN PRSS20 OR 2310015108RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Yamaguchi N., Mitsui S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Mitsui S., Yamaguchi N.;
RT "cDNA cloning of a novel brain serine protease, Hippostasin.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Blake J., Boffelli D., Bojunga N., Carinici P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

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RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mondaelet P.,
RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT *Functional annotation of a full-length mouse cDNA collection.*;
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: AB016226; BAA88825.1; -.
DR EMBL: AK009720; BAB26461.1; -.
DR EMBL: AK009360; BAB26241.1; -.
DR HSSP: P00763; IDPO.
DR MEROPS: S01.257; -.
DR MGD: MGI:1929977; Prss20.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP-Spc; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR HydroLase: Serine protease.
SQ SEQUENCE 249 AA; 27604 MW; F9FE9C8457D272D5 CRC64;

Query Match 84.5%; Score 1067; DB 11; Length 249;
Best Local Similarity 81.3%; Pred. No. 1.8e-103;
Matches 187; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

QY 1 RIKEGECRHSQPMQALFEKTRLLCGATLLAPRMLLTAHCLKRYIVHLCOHNLQKE 60
DB 20 RIKEGECRHSQPMQVAFQKTRLLCGATLLAPRMLLTAHCLKRYIVHLCOHNLQKE 79
QY 61 EGCEQRTATESPPHGFNNSLPNKDRNDIMLVKMASPVSIWAVRPLTSSRCYTAGT 120
DB 80 DGCEQRMATESPPHGFNNSLPNKDRNDIMLVKMASPVFTFRVQPLTSHCHCAAGT 139
QY 121 SCLISGWSSTSPQLRPLRLPRLRCANTITIEHOKCENAYPGNITDTWVCASVQEGKDSQ 180
DB 140 SCLISGWSSTSPQLRPLRLPRLRCANYSITIEHKECEKAYNGNITDTWVCASVREKGDSCQ 199
QY 181 GDSGGLVNCNSLQGIISWGDCPCATRKRGVYTKYCKYVDWIOETMKN 230
DB 200 GDSGGLVNCNSLQGIISWGDCPCAVTRKRGVYTKYCKYFNMVHEWRNN 249

RESULT 2
Q9QYN3 PRELIMINARY; PRT; 276 AA.
ID Q9QYN3;
AC Q9QYN3;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hipostasin prostate type.
DE PRSS20.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Yamaguchi N., Mitsui S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Mitsui S., Okui A., Komiyama K., Demura H., Yamaguchi N.;
RT *cDNA cloning and tissue-specific splicing variants of mouse

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RT hipostasin/TISP (PRSS20).";
RL Biochim. Biophys. Acta 1494:206-210(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: AB016227; BAA36955.1; -.
DR HSSP: P00763; IDPO.
DR MEROPS: S01.257; -.
DR MGD: MGI:1929977; Prss20.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP-Spc; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR HydroLase: Serine protease.
SQ SEQUENCE 276 AA; 30753 MW; 90BDC03A8AB178D6 CRC64;

Query Match 84.5%; Score 1067; DB 11; Length 276;
Best Local Similarity 81.3%; Pred. No. 2e-103;
Matches 187; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

QY 1 RIKEGECRHSQPMQALFEKTRLLCGATLLAPRMLLTAHCLKRYIVHLCOHNLQKE 60
DB 47 RIKEGECRHSQPMQVAFQKTRLLCGATLLAPRMLLTAHCLKRYIVHLCOHNLQKE 106
QY 61 EGCEQRTATESPPHGFNNSLPNKDRNDIMLVKMASPVSIWAVRPLTSSRCYTAGT 120
DB 107 DGCEQRMATESPPHGFNNSLPNKDRNDIMLVKMASPVFTFRVQPLTSHCHCAAGT 166
QY 121 SCLISGWSSTSPQLRPLRLPRLRCANTITIEHOKCENAYPGNITDTWVCASVQEGKDSQ 180
DB 167 SCLISGWSSTSPQLRPLRLPRLRCANYSITIEHKECEKAYNGNITDTWVCASVREKGDSCQ 226
QY 181 GDSGGLVNCNSLQGIISWGDCPCATRKRGVYTKYCKYVDWIOETMKN 230
DB 227 GDSGGLVNCNSLQGIISWGDCPCAVTRKRGVYTKYCKYFNMVHEWRNN 276

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RESULT 3
Q96R00 PRELIMINARY; PRT; 255 AA.
ID Q96R00;
AC Q96R00;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Prostloogen.
DE Prostloogen (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21226193; PubMed=11327827;
RA Takayama T.K., Carter C.A., Deng T.;
RT *Activation of prostate-specific antigen precursor (pro-PSA) by
RT prostin, a novel human prostatic serine protease identified by
RT RT deenerate PCR.*;
RT Biochemistry 40:1679-1687(2001).
DR EMBL: AF303046; AAK62813.1; -.
DR MEROPS: S01.081; -.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR HydroLase: Serine protease.
SQ SEQUENCE 255 AA; 27986 MW; 00D5B79E14B9468F CRC64;

Query Match 53.9%; Score 681; DB 4; Length 255;
Best Local Similarity 51.7%; Pred. No. 4.3e-63;
Matches 124; Conservative 36; Mismatches 66; Indels 14; Gaps 3;

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QY 1 RIIFGECKRHSOPWQALAEKTRLLCGATLIAPRWLLTAHCLKPRVYIHLGCHNLOKE 60
D 20 KLEGGDCAPHSOPWQALAEKTRLLCGATLIAPRWLLTAHCLKPRVYIHLGCHNLOKE 79
QY 61 EGCEQRTATESPFPHPFNNSLPKNDHNDIMLVKMASPVSIIMAVPRLTLSSRCVYAGT 120
D 80 DGEQQLTLVTIDFFPFPFNNSLPKNDHNDIMLVKMASPVSIIMAVPRLTLSSRCVYAGT 135
QY 121 SCLISGWSSTSPOLRLPHRLRCANITITIEHOKENAYPCNITPTWMCAS 170
D 136 ACVYSGMGLVSHNPEGRASPRGVSLLPDLHLCANIGIISDTSCDKYPRGLNTWMCAG 195
QY 171 VQESGKDSGCGSGPLVNCOSLOGIISWQDPCATRRKGVYTKVCKYVDWIQETKNN 230
D 196 AEGRGASCSGDSGGLVCGIILQGIIVSGWGDPCDNTTKRGVYTKVCKYVDWIQETKNN 255

RESULT 4
Q9DB08 PRELIMINARY; PRT; 251 AA.
ID 09DB08
AC 09DB08;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 1200016C12Rik protein.
GN 1200016C12Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LUNG;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J.H., Kohsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC EMBL: AK004807; BAB23579.1; -
CC HSSP: P00763; IDPO.
CC MEROPS: S01.307; -
DR MGD: MGI:1921082; 1200016C12Rik.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYPSIN_DOM; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Hydrolyase; Serine protease.
SQ SEQUENCE 251 AA; 2815 MW; F4D667F8C80C4A23 CRC64;

Query Match 50.0%; Score 632; DB 11; Length 251;
Best Local Similarity 51.7%; Pred. No. 5, 6e-58;
Matches 119; Conservative 37; Mismatches 74; Indels 0; Gaps 0;

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QY 1 RIIFGECKRHSOPWQALAEKTRLLCGATLIAPRWLLTAHCLKPRVYIHLGCHNLOKE 60
D 22 RAVGARCVRNNSXPMWAGLFYTRQGLCATLIINQWLLTAHCKRPLVWRGLGHLMRW 81
QY 61 EGCEQRTATESPFPHPFNNSLPKNDHNDIMLVKMASPVSIIMAVPRLTLSSRCVYAGT 120
D 82 EGPEQLTLVTIDFFPFPFNNSLPKNDHNDIMLVKMASPVSIIMAVPRLTLSSRCVYAGT 141
QY 121 SCLISGWSSTSPOLRLPHRLRCANITITIEHOKENAYPCNITPTWMCAS 180
D 142 QCLIFGWSVSSKQYPMQLQCANISILDNKFCRMVYPGIIFKRLCAGLMEGGRSQ 201
QY 181 GDSGGLVNCOSLOGIISWQDPCATRRKGVYTKVCKYVDWIQETKNN 230
D 202 GDRGGLVNCOSLOGIISWQDPCATRRKGVYTKVCKYVDWIQETKNN 251

RESULT 5
Q9D140 PRELIMINARY; PRT; 293 AA.
ID 09D140
AC 09D140;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 1110030019Rik protein.
GN 1110030019Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J.H., Kohsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC EMBL: AK003996; BAB23113.1; -
CC HSSP: P00763; IDPO.
CC MEROPS: S01.418; -
DR MGD: MGI:1915918; 1110030019Rik.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYPSIN_DOM; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease.
SQ SEQUENCE 293 AA; 31908 MW; ED1F45D8226FE911 CRC64;

Query Match 49.8%; Score 628.5; DB 11; Length 293;

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QY 1 RIINGECKRHSQWQALAEKTLGATLIAPRMLITAAHCLKPRYIHLGCHNIQKE 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 23 KIVGGYTCRENSIPYQVSL-NSGYHFCGSLINDQWVVAHAHCYKTRIOVLEGHINIVL 81
QY 61 EGCQOTRATESPFPHPGNNSLPKHNRNDIMLVKMAFPSITWAVRPLTSSRCVYAGT 120
   || || || || || || || || || || || || || || || || || || || || ||
Db 82 EGNQFIDAKKIHKHPNFRKTLN----NDIMLKISSPYTLNARVATVALPSSCAAGT 137
QY 121 SCLISGWSSTSPQLRLPHRLCANITITIEHOKCENAYPGNITDPMVCASVOEGKDSQC 180
   || || || || || || || || || || || || || || || || || || || || ||
Db 138 QCLISGNGNTLSFGVSRPDLQCLDAPLLPQADCEASYPGKITNNMVCAGLEGKDSQC 197
QY 181 GDSCGPLVCNOSLOGIISWGDPCATIRKPGCVYTKVKYVDIOWIETMKN 230
   || || || || || || || || || || || || || || || || || || || || ||
Db 198 GDSCGPLVCNOLQIVSWGYG-CALPDNPGVYTKVCNYVDIOWIETIAAN 246

RESULT 8
Q90UK9 PRELIMINARY; PRT; 246 AA.
ID 01-MAY-2000 (Tremblrel. 13, Created)
AC Q90UK9;
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE TSP4 (0910001B19RIK protein) (Trypsinogen 9).
GN TC OR 0910001B19RIK OR TRYPSINOGEN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=99436155; PubMed=10506205;
RA Ohmura K., Kohno N., Kobayashi Y., Yamagata K., Sato S.,
RA Kashiwabara S., Baba T.;
RT "A homologue of pancreatic trypsin is localized in the acrosome of
RT mammalian sperm and is released during acrosome reaction.";
RL J. Biol. Chem. 274:29426-29432(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carrincci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita W., Gariboldi M.,
RA Guslinich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=2103195; PubMed=11160223;
RA Chen F., Rowen L., Hood L., Rothenberg E.V.;
RT "Differential transcriptional regulation of individual TCR Vbeta
RT segments before gene rearrangement.";
RL J. Immunol. 166:1771-1780(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.

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DR EMBL: AB009661; BAA85187.1; -.
DR EMBL: AB017031; BAA74760.1; -.
DR EMBL: AK007843; BAB25300.1; -.
DR EMBL: AE000664; AAB69057.1; -.
DR HSSP: P00763; 1DPO.
DR MEROPS: S01.058; -.
DR MGD; MGI:1913350; 0910001B19RIK.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser. protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR KMW: Hydrolase. Serine protease.
SQ SEQUENCE 246 AA; 26277 MW; 915C92353EC42809 CRC64;

Query Match 46.7%; Score 590; DB 11; Length 246;
Best local similarity 48.7%; Pred. No. 1.4e-53;
Matches 112; Conservative 36; Mismatches 76; Indels 6; Gaps 3;

QY 1 RIINGECKRHSQWQALAEKTLGATLIAPRMLITAAHCLKPRYIHLGCHNIQKE 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 23 KIVGGYTCRENSIPYQVSL-NSGYHFCGSLINDQWVVAHAHCYKTRIOVLEGHINIVL 81
QY 61 EGCQOTRATESPFPHPGNNSLPKHNRNDIMLVKMAFPSITWAVRPLTSSRCVYAGT 120
   || || || || || || || || || || || || || || || || || || || || ||
Db 82 EGNQFIDAKKIHKHPNFRKTLN----NDIMLKISSPYTLNARVATVALPSSCAAGT 137
QY 121 SCLISGWSSTSPQLRLPHRLCANITITIEHOKCENAYPGNITDPMVCASVOEGKDSQC 180
   || || || || || || || || || || || || || || || || || || || || ||
Db 138 QCLISGNGNTLSFGVSRPDLQCLDAPLLPQADCEASYPGKITNNMVCAGLEGKDSQC 197
QY 181 GDSCGPLVCNOSLOGIISWGDPCATIRKPGCVYTKVKYVDIOWIETMKN 230
   || || || || || || || || || || || || || || || || || || || || ||
Db 198 GDSCGPLVCNOLQIVSWGYG-CALPDNPGVYTKVCNYVDIOWIETIAAN 246

RESULT 9
Q9ROT7 PRELIMINARY; PRT; 246 AA.
ID 01-MAY-2000 (Tremblrel. 13, Created)
AC Q9ROT7;
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE TSP4 (0910001B19RIK protein) (Trypsinogen 8).
GN TD OR 0910001B19RIK OR TRYPSINOGEN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129SVJ;
RX MEDLINE=99436155; PubMed=10506205;
RA Ohmura K., Kohno N., Kobayashi Y., Yamagata K., Sato S.,
RA Kashiwabara S., Baba T.;
RT "A homologue of pancreatic trypsin is localized in the acrosome of
RT mammalian sperm and is released during acrosome reaction.";
RL J. Biol. Chem. 274:29426-29432(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=STOMACH AND SPLEEN;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

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RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shidata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Watanabe-Borls A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Yashizaki Y.,
 RA *Functional annotation of a full-length mouse cDNA collection.*;
 RT Nature 409:685-690(2001).
 RL [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=21103195; PubMed=11160223;
 RA Chen F., Rowen L., Hood L., Rothenberg E.V.;
 RT "differential transcriptional regulation of individual TCR beta
 RT segments before gene rearrangement.";
 RL J. Immunol. 166:1771-1780(2001).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL: AB017032; BAA74761.1; -;
 DR EMBL: AK008667; BAB25821.1; -;
 DR EMBL: AK003064; BAB2542.1; -;
 DR EMBL: AE000664; AAB69056.1; -;
 DR HSSP: P00763; 1SLU.
 DR MEROPS: S01.057; -;
 DR MGD: MG1:1913350; 0910001B19RLK.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYSP-SPC; 1.
 DR PROSITE: PS00134; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Serine protease.
 KW SEQUENCE 246 AA; 26274 MW; B6A9FAC9079633F CRC64;
 SQ

Query Match 46.6%; Score 589; DB 11; Length 246;
 Best Local Similarity 48.7%; Pred. No. 1.7e-53;
 Matches 112; Conservative 35; Mismatches 77; Indels 6; Gaps 3;

QY 1 RIIFGECKPHSOPWQALFEKTRLLCGATLLAPRWLLTAHCKRPYIVHGOHMOKE 60
 DB 23 KIYGYTCRENSVYQVSL-NSGYHFCGSLINDQVNSAHCYKSRIOVRGEHNINVL 81
 QY 61 EGCEQRTATSESPHPGF-----NNSLPNKDRNDIMLVKASPVSTWAVRPLTSSRCTACT 120
 DB 82 ENEQGFVNSAKTIKHPNFNSRLN---NDIMLIKLASPVTLNARVATVALLPSSCAPAGT 137
 QY 121 SCLISGWSSTSPQLRPLPTLRCAITTEIHOKECENAYPGNTIDTWVCASVOEGGDSQO 180
 DB 138 QCLISGWSMTLSFGVNNPDLQCLAPLPLPADCEASVYCKITNNICVGFLEGGDSQO 197
 QY 181 GDSGGLVNCOSLQGIISGWDPCATITRPGVYTKVCKYVDMIOETMKN 230
 DB 198 GDSGGLVNCOSLQGIISGWDPCATITRPGVYTKVCKYVDMIOETMKN 246

RESULT 10
 O63275 PRELIMINARY; PRT; 239 AA.
 AC O63275;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE Kallikrein (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SUBMANDIBULAR GLAND;
 RA Zintz C.B., Ma J.-X., Chao J., Chao L.;
 RT "Isolation and characterization of a new rat kallikrein cDNA with
 RT predominant expression in the kidney.";
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL: L3840; AAS58782.1; -;
 DR HSSP: P00759; 1TON.
 DR MEROPS: S01.411; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYSP-SPC; 1.
 DR PROSITE: PS00134; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Serine protease.
 KW NON_TER 1
 KW SEQUENCE 239 AA; 26382 MW; 3CBD761AF06ABB53 CRC64;
 SQ

Query Match 46.6%; Score 588.5; DB 11; Length 239;
 Best Local Similarity 44.9%; Pred. No. 1.9e-53;
 Matches 106; Conservative 46; Mismatches 73; Indels 11; Gaps 3;

QY 1 RIIFGECKPHSOPWQALFEKTRLLCGATLLAPRWLLTAHCKRPYIVHGOHMOKE 60
 DB 8 RVYGGFKCKNSOPWQAVAINED--LCGVLLDPSWVITAAHCYSNDNHVLLGNNLSHD 65
 QY 61 EGCEQRTATSESPHPGF-----NNSLPNKDRNDIMLVKASPVSTWAVRPLTSSRCTACT 114
 DB 66 ---VQRLVNSQSPRHPDYKPLRNHTRKPKYNDMLHLHSEPADIDGKVIDLPK 122
 QY 115 CYTAGTSCISGWSSTSPQLRPLPTLRCAITTEIHOKECENAYPGNTIDTWVCASVOEG 174
 DB 123 EPRVSGTCLVSGSTNPSEWEPDQCVNIHLSENKICAKYKEXYDMLCAGELGG 182
 QY 175 GDSGGLVNCOSLQGIISGWDPCATITRPGVYTKVCKYVDMIOETMKN 230
 DB 183 GDTGCGDSGGLICDGLVIGITWSVPCGPBNKRGVITKLFYSWIKEMKKN 238

RESULT 11
 O63274 PRELIMINARY; PRT; 235 AA.
 AC O63274;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE Kallikrein (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;
 RA Zintz C.B., Ma J.-X., Chao J., Chao L.;
 RT "Isolation and characterization of a new rat kallikrein cDNA with
 RT predominant expression in the kidney.";
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL: L3839; AAS58781.1; -;
 DR HSSP: P00759; 1TON.
 DR MEROPS: S01.410; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 14:16:02 ; Search time 50 Seconds

(without alignments)
442.218 Million cell updates/sec

Title: US-09-856-320A-2_COPY_53_282

Perfect score: 1263

Sequence: 1 RIIRKFECKPHSQPMQALF.....GYTTKVKCYDWTQETMKN 230

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	686	54.3	260	2	neuropilin - mouse
2	610.5	48.3	265	1	KORP
3	605.5	47.9	261	2	A31136
4	600.5	47.5	261	1	NGMSG
5	596.5	47.2	263	2	S15686
6	596	47.2	248	2	S55066
7	593	47.0	246	1	TRRT2
8	590.5	46.8	261	2	A34079
9	590	46.7	238	2	S31779
10	589	46.6	246	1	TRRT1
11	586.5	46.4	259	2	B31136
12	582.5	46.1	261	2	A29586
13	582.5	46.1	261	2	A29745
14	579.5	45.9	261	2	S45303
15	579	45.8	231	1	TRPGPR
16	578	45.8	232	1	KOPG
17	573	45.4	246	2	B25528
18	572.5	45.3	259	1	KORTTN
19	570.5	45.2	261	2	A25606
20	570	45.1	247	1	TRDG
21	569.5	45.1	244	2	A44284
22	569.5	45.1	261	1	KOMS1
23	567	44.9	262	1	KOHU
24	566	44.8	229	1	TRB0TR
25	562	44.5	248	2	S55067
26	561.5	44.5	257	2	S33772
27	561.5	44.5	261	2	S01971
28	558	44.2	243	2	A35871
29	558	44.2	247	2	S13813

30	556.5	44.1	261	1	A32297	semenogelase (EC 3
31	555	43.9	247	2	A27547	trypsin (EC 3.4.21
32	554.5	43.9	231	2	S31778	trypsin (EC 3.4.21
33	554.5	43.9	247	2	S05494	trypsin (EC 3.4.21
34	553.5	43.8	259	2	A29746	tissue kallikrein
35	553.5	43.8	261	1	S35711	semenogelase (EC 3
36	553.5	43.8	261	2	A41020	tissue kallikrein
37	552	43.7	246	1	TRDGC	tissue kallikrein
38	552	43.7	256	1	NGMSA	75 nerve growth fa
39	551.5	43.7	239	2	A27207	tissue kallikrein
40	548.5	43.4	261	2	JE0236	tissue kallikrein
41	548	43.4	253	2	A53968	serine proteinase
42	547.5	43.3	261	1	TRMSMS	tissue kallikrein
43	546.5	43.3	242	2	S31775	trypsin (EC 3.4.21
44	546.5	43.3	242	2	S49489	trypsin (EC 3.4.21
45	546.5	43.3	242	2	S31776	trypsin (EC 3.4.21

ALIGNMENTS

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RESULT 1
156559
neuropilin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: 156559
R:Chen, Z.L., Yoshida, S., Kato, K., Momota, Y., Suzuki, J., Tanaka, T., Ito, J., Nis
J. Neurosci. 15, 5088-5097, 1995
A:Title: Expression and activity-dependent changes of a novel limbic-serine protease
A:Reference number: 156559; M01D:5348817; PMID:7623137
A:Accession: 156559
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-260 <RES>
A:Cross-references: GB:D30785; NID:g1648847; PIDN:BA06451.1; PID:g1020091
C:Superfamily: trypsin; trypsin homology
F:33-252/Domain: trypsin homology <TRY>

Query Match          54.3%  Score 686; DB 2; Length 260;
Best Local Similarity 52.8%  Pred. No. 1.9e-53;
Matches 121; Conservative 36; Mismatches 70; Indels 2; Gaps 2;

QY 1 RIIRKFECKPHSQPMQALFETRLCGATLIAPRWLITAAHCLKPRYIVHIGQHNLOKE 60
DB 32 KILRGECIPHSQPMQALFQGERLIGCVLWGRWVLTAAHCKKQKVSRLGSHSIQSR 91
QY 61 EGCQTRATSEFHPGNNSLPKNDHRNDIMLYKMASPVSTIYAVRPLTSSRCVYAGT 120
DB 92 DQPEQIOVAOSIQHPCCYNNSNP-EDHSHDITMLRLQNSANLGDVKVQPLANLCPKVQ 150
QY 121 SCLISGMSGTSPOLRLPHTLRCAINTITIEHCKENAVPGNITDMWCAVQEGSKDSQ 180
DB 151 KCIISGKGVTSFQBNFNPNTLNCALFVKIYSQNKCEKRAVPGITBEMVACAG-SSMGADTCQ 209
QY 181 GDSCGPIVCDMGLGITSWGSDDPCGKPEKPGVYTRIKICVTTWIKKTYMDN 258
DB 210 GDSCGPIVCDMGLGITSWGSDDPCGKPEKPGVYTRIKICVTTWIKKTYMDN 258

RESULT 2
KORP
tissue kallikrein (EC 3.4.21.35) precursor - rat
N:Alternate names: glandular kallikrein; kininogenin; true tissue kallikrein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 16-Jun-2000
C:Accession: A00944; A41429; A25137; JX0073; A23863; A33359
R:Swift, G.H.; Dagorn, J.C.; Ashley, P.L.; Cummings, S.W.; MacDonald, R.J.
Proc. Natl. Acad. Sci. U.S.A. 79, 7267-7267, 1982
A:Title: Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid sequence
A:Reference number: A00944; M01D:53117659; PMID:6961406
A:Accession: A00944
A:Molecule type: mRNA
```

```

A:Residues: 1-265 <SWI>
A:Experimental source: pancreatic
R:Kato, H.; Nakanishi, E.; Enjyoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biochem. 102, 1389-1404, 1987
A:Title: Characterization of serine proteinases isolated from rat submaxillary gland: w
A:Reference number: A41429; PMID:88198057; PMID:3482210
A:Accession: A41429
A:Status: preliminary
A:Molecule type: protein
A:Residues: 29-53, 'X', 55-87 <KAT>
R:Gerald, W.L.; Chao, J.; Chao, L.
Biochem. Biophys. Acta 866, 1-14, 1986
A:Title: Immunological identification of rat tissue kallikrein cDNA and characterization
A:Reference number: A25137; PMID:86131678; PMID:3004582
A:Accession: A25137
A:Molecule type: mRNA
A:Residues: 115-265 <GER>
R:Inoue, H.; Fukui, K.; Miyake, Y.
J. Biochem. 105, 834-840, 1989
A:Title: Identification and structure of the rat true tissue kallikrein gene expressed
A:Reference number: JX0073; PMID:89327211; PMID:2753879
A:Accession: JX0073
A:Molecule type: DNA
A:Residues: 1-265 <INO>
A:Cross-references: GB:D00448; NID:g220792; PIDN:BA00346.1; PID:g220794
A:Experimental source: Kidney
R:Ashley, P.L.; MacDonald, R.J.
Biochemistry 24, 4512-4520, 1985
A:Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of
A:Reference number: A23863; PMID:86091477; PMID:2998455
A:Accession: A23863
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-265 <ASH>
A:Cross-references: GB:M1563; NID:g205029; PIDN:AAA1464.1; PID:g205030
A:Experimental source: submaxillary gland
R:Wines, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; MacDonald, R.J.
J. Biol. Chem. 264, 7653-7662, 1989
A:Title: Organization and expression of the rat kallikrein gene family.
A:Reference number: A33359; PMID:89214217; PMID:2708383
A:Accession: A33359
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 5-265 <MIN>
A:Cross-references: GB:M23874; GB:J04701; GB:M23875; GB:M23876; NID:g205007; PIDN:AAA14
A:Comment: The kallikreins liberate lysyl-bradykinin, a vasoactive decapeptide, from kin
C:Comment: The protein presumably assumes the two-chain form by cleavage between residu
C:Comment: tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release
C:Genetics:
A:introns: 20/1, 73/2, 169/1, 214/3
C:Superfamily: trypsin, trypsin homology
C:Keywords: hydrolase; pancreas; serine proteinase; zymogen
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-28/Domain: activation peptide #status predicted <ACT>
F:29-265/Product: tissue kallikrein, pancreatic #status predicted <MP>
F:29-257/Domain: trypsin homology <TRY>
F:35-177, 54-70, 156-223, 188-202, 213-238/Disulfide bonds: #status predicted
F:69, 124, 217/Active site: His, Asp, Ser #status predicted

Query Match 48.3%; Score 610.5; DB 1; Length 265;
Best Local Similarity 45.6%; Pred. No. 9, 8e-47;
Matches 108; Conservative 43; Mismatches 79; Indels 7; Gaps 1;

```

```

DB 148 EEPKVGSTCLASGWSITPDCLEISDDLOQCNIDLSNEKCEVNAHKEEYTDLMLCAGEND 207
QY 174 GGRDSCGDSGCPVLCNOSLOGIIISMGDPCATRRKRGVYTKCKYVDWIOETMKN 230
DB 208 GGRDTCGDSGCPVLCNOSLOGIIISMGDPCATRRKRGVYTKCKYVDWIOETMKN 264

RESULT 3
A31136
tissue kallikrein (EC 3.4.21.35) 7 precursor, submandibular - rat
N:Alternate names: glandular prokallikrein 7, submandibular, proteinase A
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1990 #sequence, revision 31-Mar-1990 #text-change 22-Jun-1999
C:Accession: A31136; S10698; S10699; D41429; B41429; S09315
R:Chen, Y.P.; Chao, J.; Chao, L.
Biochemistry 27, 7189-7196, 1988
A:Title: Molecular cloning and characterization of two rat renal kallikrein genes.
A:Reference number: A31136; PMID:89088074; PMID:2849988
A:Accession: A31136
A:Molecule type: DNA
A:Residues: 1-261 <CHE>
A:Cross-references: GB:M19647; GB:J02837; NID:g204999; PIDN:AAA1461.1; PID:g205000
R:Elmoujahed, A.; Gutman, N.; Brillard, M.; Gauthier, F.
FEBS Lett. 265, 137-140, 1990
A:Title: Substrate specificity of two kallikrein family gene products isolated from t
A:Reference number: S10698; PMID:90306305; PMID:2194829
A:Accession: S10698
A:Molecule type: protein
A:Residues: 25-36 <ELM>
A:Accession: S10699
A:Molecule type: protein
A:Residues: 112-139 <ELD>
R:Kato, H.; Nakanishi, E.; Enjyoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biochem. 102, 1389-1404, 1987
A:Title: Characterization of serine proteinases isolated from rat submaxillary gland:
A:Reference number: A41429; PMID:88198057; PMID:3482210
A:Accession: A41429
A:Molecule type: protein
A:Residues: 112-133 <KAT>
A:Accession: B41429
A:Molecule type: protein
A:Residues: 25-34, 'D', 36-45, 'S', 47-67, 'X', 69-75 <KA2>
R:Brady, J.M.; MacDonald, R.J.
Arch. Biochem. Biophys. 278, 342-349, 1990
A:Title: The expression of two kallikrein gene family members in the rat kidney.
A:Reference number: S09315; PMID:90225801; PMID:2183721
A:Accession: S09315
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 43-45, 'S', 47-114, 'A', 116-261 <BRA>
C:Superfamily: trypsin, trypsin homology
C:Keywords: hydrolase; signal sequence #status predicted <SIG>
F:1-18/Domain: signal sequence #status predicted <ACT>
F:19-261/Product: tissue prokallikrein 7, submandibular #status predicted <KAT>
F:25-253/Domain: trypsin homology <TRY>
F:65, 120, 213/Active site: His, Asp, Ser #status predicted

Query Match 47.9%; Score 605.5; DB 2; Length 261;
Best Local Similarity 46.4%; Pred. No. 2, 7e-46;
Matches 110; Conservative 39; Mismatches 81; Indels 7; Gaps 1;

```

```

Qy 174 GGDSCQGDSSGGPLYCNO$SLGIISMGDPCAITRPGVYTKYCKYVDWJQETMKN 230
      |||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 204 GCKDTGSDSGGPGLLCDGVLQGITSMG$VPCAKTNMPAIYTKLIKFTSWIEVMKN 260

```

RESULT 4

7S nerve growth factor gamma chain (EC 3.4.21.-) precursor - mouse
C:Species: Mus musculus (house mouse)

C;Date: 18-Dec-1981 #sequence_revision 17-May-1985 #text_change 18-Jun-1999
C;Accession: A91005; A90949; A93510; A92341; A00942; A21093; A22705
R;Evans, B.A.; Richards, R.I.

EMBO J. 4, 133-138, 1985
A:Title: Genes for the alpha and gamma subunits of mouse nerve growth factor are contig
R:Reference number: A91005; MUID:85257431; PMID:3848399

A:Accession: A91005
A:Molecule type: DNA
A:Residues: 1-261 <EVA>
B:Ritch A A Crow A Wood B T. Harefield T. Gephart D. H

A:Title: Isolation of a cDNA clone coding for the gamma-subunit of mouse nerve growth factor
A:Reference number: A90949; MUID:85076169; PMID:6548955
A:Accession number: 300040
A:Publication: 1984
A:Author: KOLLICHN, A.; GRAY, A.; WOOD, W.L.; HAYLICK, J.; SEEBURG, P.H.
A:Page: 387-392, 1984

A;Accession: A90949
A;Molecule type: mRNA
A;Residues: 1-261 <U>
A;Cross-references: CB

Title: Use of a cDNA recombinant for the gamma-subunit of mouse gamma-glutamyl transaminase

References: GB:A01359; MD:953373; PIDN:CAZ5845.1; PID:g533/4
R;Howles, P.N.; Dickinson, D.P.; DiCaprio, L.L.; Woodworth-Gutai, M.;
Nucleic Acids Res. 12, 2791-2805, 1984

A: Molecule type: mRNA
A: Accession: A93510
A: Reference number: A93510; PMID:6200835
A: Article: use of a cDNA recombinant for the gamma subunit of mouse nerve growth factor

A;Residues: 127-202, 'E', 204-261 <HOW>
A;Cross-Preferences: GB:X00472; MID:g54260; PIDN:CAA25154.1; PID:g54261
Experimental source: Inbred strain DBA/2J

R; Thomas, K. A.; Baglan, N. C.; Bradshaw, R. A. J. Biol. Chem. 256, 9156-9166, 1981

A;Reference number: A92341; MUID:81264363; PMID:7263706
A;Accession: A92341
A;Molecule type: protein

A;Residues: 25-107,112-261 <THO>
A;Experimental source: outbred s
C;Comment: 7S nerve growth facto

C;Comment: The active form of the gamma chain occurs naturally as combinations of either C;Genetics: 7
A;Map position: 7

A; Introns: 16/1; 69/2; 165/1; 210/3
C; Superfamily: trypsin; trypsin homology
C; Keywords: glycoprotein; growth factor;

F:1-18/Domains: signal sequence #status predicted <SIG>
E:25-253/Domains: trypsin homology <TRY>
F:25-107/Domains: segment B1 <GB1>

```

E:25-107,112-261/Product: nerve growth factor gamma chain (active form) #status experiment
E:112-261/Domain: segment A <GAA>
F:112-164/Domain: segment C <GCC>

```

F:165-261/Domain: segment B2 <GB2>
F:31-173, 50-66, 152-219, 184-198, 209-234/Disulfide bonds: #status predicted
F:65, 120, 213/Active site: His, Asp, Ser #status predicted

Query Match	Score	DB 1	Length	261
F:102/Binding site: carbohydrate (Asn) (covalent) #status experimental	47.58			

	Best Local Similarity	44.7%;	Pred. No.	7.4e-46;			
	Matches	106;	Conservative	46; Mismatches	78; Indels	7; Gaps	1;

DQ 1 RIKGFECKRHSQPWQAALFEKIRLLCGATLIAPRUULTAAHCLKPRIVLHGHNLOKE 60
||::|:::||| |:: |::| |::|::|::|::|::|::|::|::|::|::|::|::|:
Db 24 RIVGGECKEKNSQPMWHAVRYTYQLCGVLLDPNMVLTAAHCYDDNYKVMLGNNLFKD 83

```

0y      61 ECGETRATESPPHGFNNSLPNK-----DHRNDIMLVKMASPVSTWAVRPLTSS 113
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
0b      64 FPGNUPHETGKATINDCENUTMREYUWDEYEDUCNDVUTETCTGNDCTDCTDCTCTCTCT 143

```

[illegible]

RESULT 5

CtSpecies: Mastomys natalensis
CtSpecies: Mastomys natalensis precursor, renal - multimammate rat (Mastomys natalensis)
CtSpecies: Mastomys natalensis

C:Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: I83227; SI5686
R:Fahnestock, M.
DNA Cell Biol 13 293-300 1994

DNA Cell Biol. 13, 253-300, 1994
 Article Characterization of kallikrein cDNAs from the African rodent Mastomys
 A. Reference number: 160208; MUID:94226702; PMID:7909667
 Accession: 1A1327

A:Residues: 1-263

A:Cross-references: EMBL:X17352; NID:g55526; PIDN:CAA35232.1; PID:g55527
C:Superfamily: trypsin homology
C:Keywords: hydrolyase; serine protease
C:Keywords: trypsin; trypsin homology

F;25-255/Domain: trypsin homology <TRY>
F;65,121,215/Active site: His, Asp, Ser #status predicted

Query Match	47.28	Score 596.5	DB 2	Length 263
Best Local Similarly	44.88	Pred. NO. 1.7e-45		
Matches 107; Conservative	44	Mismatches 79	Indels 9	Gaps 2

0Y 1 RIKGECKPHSOPMOALFEKTRLLGATLLAPRWLTAHCLIPRYIYLGOHNLQKE 60
||| ||| : ||| |:: | | : |: ||| ||| : | | ||| ::

Db 24 RIIGFNCERNKNSQPMHVAVYREARYQCGGVLIDANWVLTAAHCYNDKYQVWLGNRRFED 83

Qy 61 EGCQOTRTATESFPHPHGFNNLSLPNKDH-----RNDIMLVKMASPVSLTWAVRPILTSL 112

```

      | : :: ||||| || |||      ||::||: | || :|: |
Db    84 EPSAOHQLSKAIPHGFNMSLINKDHTPHPEDDYNDIMLVRLKKAPEITDVVKPIDLP 143

```

```

0y 113 SRCVTAAGTSCILSGWSTS -SPQLRPHTLRCANITIEHOKCENAYPGNITDTMWCASV 171
      : | : | | | | | : : | : | : : : | : : | | | | |
Db 144 TEETVGSRCILASGWSSTPTEEFESHDLQCYLELLSNEVCAKAHTEKVTDTMTCAGE 203

```

172 QEGKDCQGSGLPYCNSLOGIISWGDPCATRKPGVYTKVKCYVDWIQETMKNN 230

RESULT 6
S55066
trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) -- chicken

N:Alternate names: trypsinogen II
C:Species: Gallus gallus (chicken)
C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999

C:Accession: S55066; S72347
R:Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995

A:Title: Isolation and characterization of the chicken tryptsinogen gene family.
A:Reference number: S55065; MUID:95251611; PMID:7733885
A:Accession: S55066
A:Medline ID: 7733885

A: Molecule type: mRNA
A: Residues: 1-248 <WANI>
A: Cross-references: EMBL:U15157; NID:g603906; PIDN:AAA7914.1; PID:g603907
A: (Cross-references) Genbank: J01003.1; DDBJ:U15157.1

A:Accession: S72347
A:Experimental source: clone Z-P29
A:Molecule type: DNA
A:Position: 1-348 (EAA3)

A:Residues: 1-246 (SWAN2)
A:Cross-references: EMBL:U15157; NID:g603906; PIDN:AAA79914.1; PID:g603907
A:Experimental source: clone 2-P29
C:Superfamily: trvnsin; trvnsin homolog

Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen

A:Accession: S66657
A:Molecule type: mRNA
A:Residues: 1-238 <MAL>
A:Cross-references: EMBL:X70074, NID:g64387, PIDN:CAA9679.1, PID:g64388
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine protease
F:1-7/Domain: signal sequence (prosegment) #status predicted <SI>
F:8-15/Domain: activation peptide (prosegment) #status predicted <AP>
F:16-238/Product: trypsin fii #status predicted <MAN>
F:16-231/Domain: trypsin homology <TRY>
F:12-152,40-56,124-225,131-198,163-177,188-212/Disulfide bonds: #status predicted
F:53,99,192/Active site: His, Asp, Ser #status predicted

Query Match	46.78;	Score 590;	DB 2;	Length 238;
Best Local Similarity	47.88;	Pred. No. 5.7e-45;		
Matches 110; Conservative	36;	Mismatches 78;	Indels 6;	Gaps 4;

```

QY      1 RIINGEKKPHSOWMOALFEKTRILGATILAPRWITLTAANOHLKRYUYNHGOHMOKE 60
Db      15 KIVGGIECKRKRSASYQASL-QSGHFFGGSTLSTWYSAHCKYKHIOYRLDEHMAVAN 73

QY      61 EGCBOETATATESFPHGPFNNSLPNKDHARDIMLVKMASPVSTWAAVRPLTSSRCYTAGT 120
Db      74 EGTEQGLDYSVKVIMHPSYNSR--NLD--NDIMIKLSKPSALMSYSTVALPSSCASSGT 129

QY      121 SCLISGWSSTSSPOLRLPHILKCANITIIIEHOKECENAYPENITIDTWYCAVSQEGGKDSQ 180
Db      130 RCLVSGMGNLSSGSSSNYPDLRLCIDLPELTSSSCNSAYPEQOLISMNECAFMEGKGDSCQ 189

QY      181 GDSGGLPYLCNOSTLOGIISWGDGDPALIRKRGVYTKVYCYVDYDIOEMKNN 230
Db      190 GDSGGPYVVCNQLGGVYVSWGIG-CAQGNKRGVYTKVNTYMSWISSTSSNN 238

```

RESULT 10

```

trypsin (EC 3.4.21.4) I precursor - rat
N:Alternate names: trypsinogen I
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Dec-1982 #sequence.revision 17-Dec-1982 #text_change 24-Sep-1999
C:Accession: B22657; A00948
J:Cratk, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J. Biol. Chem. 259, 14255-14264, 1984
A:Title: Structure of two related rat pancreatic trypsin genes.
A:Reference number: A22657; MUID:85054880; PMID:6094547
A:Accession: B22657
A:Molecule type: DNA
A:Residues: 1-246 <CRA>
A:Cross-references: GB:J00778; NID:g206507; PIDN:AAA96518.1; PID:g206508
A:Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 17
J. Biol. Chem. 257, 9724-9732, 1982
A:Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of
A:Reference number: A00948; MUID:82265624; PMID:686710
A:Accession: A00948
A:Molecule type: mRNA
A:Residues: 1-246 <MAC>
A:Cross-references: GB:J00778; NID:g206507; PIDN:AAA96518.1; PID:g206508
C:Genetics:
A:Introns: 14/1; 67/2; 152/1; 197/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-23/Domain: activation peptide #status predicted <APT>
F:24-246/Product: trypsin I #status predicted <ENZ>
E:24-239/Domain: trypsin homology <TRY>
F:30-160,48-64,133-233,339-206,171-185/Disulfide bonds: #status predicted
F:63-107,200/Active site: His, Asp, Ser #status predicted
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 46.68; Score 589; DB 1; Length 246;
Best Local Similarity 46.38; Pred. No. 7.3e-45;
Matches 111; Conservative 35; Mismatches 78; Indels 6; Gaps 3;

```

```
QY      1 RIINGFEKPHISQWQAALKEFKFYLLCGALLIPRMYLTAHOLCKRYUYNLEJONHIJKE   60
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     23 KIVGYGICPEHSVYQVSL-NSGFHCFGSGSLINDQWVAASHCYKSRIDQIRIGEENHINVL   81

QY      61 EGCROTATESPHEPENNLSLPKHQRNDIMLYUKASPVSLIWAYPLRLTSSRCTACT   120
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     82 EGDDQFINAAKIHRHYSSWTLN----NDIMLIKSSPKVLANARAPALBPACAPAGT   137

QY     121 SCLISGWSTSSPOLRLPHILRCANITIIIEHQXCENAYPGNITDTIYWCAVSVDGGKDSQ   180
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    138 QCLISGMENTSNVNPPDLQCVDAYVLSQAOACEAAYPEETISSMIGCFEGLEGKDSCQ   197
```

```

QY      181 GDSGGPLVNCNSLGGIISMGDDPCAITRPGVYTRVCKYVDWIQETMRKN 230
          |||||:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|
Db      198 GDSGGPVCNGQLGGIVSMGTC-CALPDNPGVYTRVCKNFEVGMIDPTIAN 246

```

RESULT 11
B31136
tissue kallikrein (EC 3.4.21.35) 3 precursor, submandibular - rat
N/Alternate names: glandular prokallikrein 3, submandibular
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 22-Jun-1999
C/Accession: B31136
R/Chen, Y.P.; Chao, J.; Chao, L.
Biochemistry 27, 7189-7196, 1988
A/Title: Molecular cloning and characterization of two rat renal kallikrein genes.
A/Reference number: A31136, MUID:89086074, PMID:2849988

RESULT 11

tissue kallikrein (EC 3.4.21.35) 3 precursor, submandibular - rat
 C:Alternate names: glandular prokallikrein 3, submandibular
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #extl_change 22-Jun-1999
 C:Accession: B31136
 R:Chen, X.P., Chao, J., Chao, L.,
 Biochemistry 27, 7189-7196, 1988
 A:Title: Molecular cloning and characterization of two rat renal kallikrein genes.
 A:Reference number: A31136; M0ID:89088074; PMID:2849588
 A:Accession: B31136
 A:Molecule type: DNA
 A:Residues: 1-259 <CHE>
 A:Cross-references: GH:M19648; GB:J02837; NID:g205002; PIRD:AAA51640.1; PID:g205004
 A:Note: the authors translated the codon GTC for residue 230 as Cys
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; serine proteinase
 F:1-16/Domain: signal sequence #status predicted <Sig>
 F:19-253/Product: tissue prokallikrein 3, submandibular #status predicted <Mat>
 F:23-251/Domain: trypsin homology <Try>
 F:63,118,211/Active site: His, Asp, Ser #status predicted

Query Match	46.48;	Score 586.5;	DB 2;	Length 259;
Best Local Similarity	44.78;	Pred. No. 1.3e-44;		
Matches 106;	Conservative 39;	Mismatches 83;	Indels 9;	Gaps 2

[illegible]

RESULT 12

tissue kallikrein (EC 3.4.21.35) hCG-1 precursor - human
N:Alternate names: glandular kallikrein
C:Species: Homo sapiens (man)
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 22-Jun-1999
C:Accession: A29586
R:Schedlich, L.J.; Bennetts, B.H.; Morris, B.-J.
DNA 6, 429-437, 1987
A:Title: Primary structure of a human glandular kallikrein gene.
#:Reference number: A29586; MID:88054467; PMID:2824146

A:Accession: A29586
A:Molecule type: DNA
A:Residues: 1-261 <SCH>
A:Cross-references: GB:M18157; NID:q186640; PIDN:AAA74454.1; PID:q386842
A:Note: the authors translated the codon TAC for residue 43 as Trp
C:Genetics: 16/1; 69/2; 165/1; 210/3
A:Introns: 16/1; 69/2; 165/1; 210/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:25-253/Domain: trypsin homology <TRY>
F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 46.1%; Score 582.5; DB 2; Length 261;
Best Local Similarity 45.1%; Pred. No. 2,9e-44;
Matches 107; Conservative 42; Mismatches 81; Indels 7; Gaps 1;

OY 1 RIIGFECKPHSQPMAALFEKTRLLCGATLLPRLMILTAHCLKPRYIVHLAGOHNLQKE 60
DB 24 RIYGFCEKNSQPMVAAYRYNEYICGVLLANVLTARHCYEEENKVSLOKNNLYEE 83
OY 61 ECGEQTATATESPPHPGFNNSL-----PNKDRNDIMLVKASPVSTWAVRPLTSS 113
DB 84 EDYQGRVYSHSPHPPLKNSLTKHQSLRDEDESDHMLRLSEPAKITDVKVGLDLP 143
OY 114 RCYTAGTSCLSISGWSSTSSQQLRPHRLRCANTITIEHOCENAYRGNTIDTWVCASVOE 173
DB 144 QEPALGTCTYASGWSGSIPEPEFLRPSLQCVSLHLSNDYCARAYSEKVEFMICAGLWT 203
OY 174 GGRDSCGDSGGPGLVNCOSLOGIISWGDPACATRRKPGVYTKCKYVDVIOETMKN 230
DB 204 GGRDTCGDSGGPGLVNCVLOGITISWGCPALPEKPAVYTKVYHAKWKIDITMAN 260

RESULT 13

tissue kallikrein (EC 3.4.21.35) mGK-9 precursor, submandibular - mouse
A:Accession: A29745
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence, revision 31-Dec-1988 #text_change 22-Jun-1999
C:Accession: C29746; A29745; A27120; I70015
R:Pinkwater, C.C.; Evans, B.A.; Richards, R.I.
Biochemistry 26, 6750-6756, 1987
A:Title: Mouse glandular kallikrein genes: identification and characterization of the ge
A:Reference number: A90322; MUID:88107594; PMID:332387
A:Accession: C29746
A:Molecule type: DNA
A:Residues: 1-261 <DRI>
A:Cross-references: GB:M17985; NID:q193476; PIDN:AAA37681.1; PID:q387166
A:Experimental source: strain BALB/c, salivary gland
R:Blaber, M.; Isackson, P.J.; Bradshaw, R.A.
Biochemistry 26, 6742-6749, 1987
A:Title: A complete cDNA sequence for the major epidermal growth factor binding protein
A:Reference number: A29745; MUID:88107593; PMID:3322386
A:Accession: A29745
A:Molecule type: mRNA
A:Residues: 1-261 <BLA>
A:Cross-references: GB:M17962; NID:q192997; PIDN:AAA37541.1; PID:q309212
R:Isackson, P.J.; Silverman, R.E.; Blaber, M.; Server, A.C.; Nichols, R.A.; Shooter, E.M
Biochemistry 26, 2082-2085, 1987
A:Title: Epidermal growth factor binding protein: identification of a different protein.
A:Reference number: A27120; MUID:87299636; PMID:3304419
A:Accession: A27120
A:Molecule type: protein
A:Residues: 25-54; 112-124, 'X', 126-130; 165-184, 'X', 186-187, 'X', 189-192 <ISA>
J. Biol. Chem. 262, 8027-8034, 1987
A:Title: Mouse glandular kallikrein genes: Structure and partial sequence analysis of th
A:Reference number: I35260; MUID:87250386; PMID:3036794
A:Accession: I70015
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 70-122 <RES>
A:Cross-references: GB:M18608; NID:q198500; PIDN:AAA39351.1; PID:q198506

C:Comment: This sequence is one of approximately twenty-five members of a gene family
C:Genetics:
A:Gene: KAL
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase; zymogen
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-24/Domain: propeptide #status predicted <PRO>
F:25-261/Product: tissue kallikrein mGK-9, submandibular #status experimental <MAT>
F:25-253/Domain: trypsin homology <TRY>
F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 46.1%; Score 582.5; DB 2; Length 261;
Best Local Similarity 43.5%; Pred. No. 2,9e-44;
Matches 103; Conservative 48; Mismatches 79; Indels 7; Gaps 1;

OY 1 RIIGFECKPHSQPMAALFEKTRLLCGATLLPRLMILTAHCLKPRYIVHLAGOHNLQKE 60
DB 24 RIYGFCEKNSQPMVAAYRYNEYICGVLLANVLTARHCYEEENKVSLOKNNLYEE 83
OY 61 ECGEQTATATESPPHPGFNNSL-----PNKDRNDIMLVKASPVSTWAVRPLTSS 113
DB 84 EPSAQRVLVSKSLHPGYNRSLRHNHIREYDYSNDMLRLSKPADITDVKPIALPT 143
OY 114 RCYTAGTSCLSISGWSSTSSQQLRPHRLRCANTITIEHOCENAYRGNTIDTWVCASVOE 173
DB 144 EEPRLGSTCLASGWSSTTPPKFQNAKDQVNLKLLPNECCGAHLEKYVDVMIAGERTD 203
OY 174 GGRDSCGDSGGPGLVNCOSLOGIISWGDPACATRRKPGVYTKCKYVDVIOETMKN 230
DB 204 GGRDTCGDSGGPGLVNCVLOGITISWGCPALPEKPAVYTKVYHAKWKIDITMAN 260

RESULT 14

tissue kallikrein (EC 3.4.21.35) precursor - dog
A:Accession: S45303
C:Species: Canis lupus familiaris (dog)
C:Date: 20-Oct-1994 #sequence, revision 03-Aug-1995 #text_change 22-Jun-1999
C:Accession: S45303; S38487
R:Gautlier, E.R.; Dumas, C.; Chapdelain, P.; Tremblay, R.R.; Dube, J.Y.
Biochim. Biophys. Acta 1218, 102-104, 1994
A:Title: Characterization of canine pancreas kallikrein cDNA.
A:Reference number: S45303; MUID:94250683; PMID:8193155
A:Accession: S45303
A:Molecule type: mRNA
A:Residues: 1-261 <GND>
A:Cross-references: EMBL:X75479; NID:q414018; PIDN:CA53210.1; PID:q414019
A:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-261/Product: tissue kallikrein #status predicted <MAT>
F:25-253/Domain: trypsin homology <TRY>
F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 45.1%; Score 579.5; DB 2; Length 261;
Best Local Similarity 45.1%; Pred. No. 5,4e-44;
Matches 107; Conservative 42; Mismatches 81; Indels 7; Gaps 1;

OY 1 RIIGFECKPHSQPMAALFEKTRLLCGATLLPRLMILTAHCLKPRYIVHLAGOHNLQKE 60
DB 24 RIYGFCEKNSQPMVAALYHNSKFCGCGVIVPEVVAHAHINNOYQMLGRVLFEE 83
OY 61 ECGEQTATATESPPHPGFNNSL-----LPNKDRNDIMLVKASPVSTWAVRPLTSS 113
DB 84 EDYAGVQYRESPPHPPEFLNLSLKNTRLPEDYSDHMLRLAEPQATDVAVRVLDPT 143
OY 114 RCYTAGTSCLSISGWSSTSSQQLRPHRLRCANTITIEHOCENAYRGNTIDTWVCASVOE 173
DB 144 QEPQVSTCYASGWSIEBPKFIPDQCVDELSDNDCANAHSAQKTEFMICGHLE 203
OY 174 GGRDSCGDSGGPGLVNCOSLOGIISWGDPACATRRKPGVYTKCKYVDVIOETMKN 230
DB 204 GGRDTCGDSGGPGLVNCVLOGITISWGCPALPEKPAVYTKVYHAKWKIDITMAN 260

RESULT 15

TRPGTR

trypsin (EC 3.4.21.4) precursor - pig (tentative sequence)

N:Contains: trypsinogen

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000

C:Accession: A90641; A90368; A00947

R:Charles, M.; Rovery, M.; Guidoni, A.; Desnuelle, P.

Biochim. Biophys. Acta 69, 115-129, 1963

A:Title: Su le trypsinogene et la trypsine de porc.

A:Reference number: A90641

A:Accession: A90641

A:Molecule type: protein

A:Residues: 1-10 <CHA>

R:Hermanson, M.A.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.

Biochemistry 12, 3146-3153, 1973

A:Title: Determination of the amino acid sequence of porcine trypsin by sequenator analy

A:Reference number: A90368; MUID:73258692; PMID:4738933

A:Accession: A90368

A:Molecule type: protein

A:Residues: 9-231 <HER>

A>Note: at position 20, Ile and Val occur alternatively

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; pancreas; polymorphism; protein digestion; serine proteinase; zym

F:1-231/Product: trypsinogen #status experimental <ZYM>

F:1-8/Domain: activation peptide #status experimental <APr>

F:9-231/Product: trypsin #status experimental <MAT>

F:9-224/Domain: trypsin homology <TRY>

F:15-145,33-49,117-218,124-191,156-170,181-205/Disulfide bonds: #status predicted

F:48,92,185/Active site: His, Asp, Ser #status predicted

F:60,62,70/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 45.8%; Score 579; DB 1; Length 231;

Best Local Similarity 47.6%; Pred. No. 5.2e-44;

Matches 110; Conservative 36; Mismatches 77; Indels 8; Gaps 4;

QY 1 RIKGFECRPHSQWQALFEKRLLCATLIAPRWLITAAHCLKPRYIVHLGQHNLOKE 60

Db 8 KIVGGYTCANANSIPYQVSLNSGSH-FCGSLINSQWVSAAHCKRSRIQVRLGEHNIDVL 66

QY 61 EGCQETRTATESFPHPGFN-NSLPKDHNDIMLYKMASPVITWAVRPLTLSSRCYTAG 119

Db 67 EGNEDFTIAAKITTHPNFNGTLD---NDIMLIKISSPATLNSRVATVSLPRSCAAAG 121

QY 120 TSCLSGSGSTSPQLRLPHTLRACANITRIEHQKCNAYPGNITPDYWCASVOEGKDC 179

Db 122 TBCLSGSGNTKSSGSSIFSLQCLAKAPVLSDSCKSSYPGQITGNMTCVGFLEGKDC 181

QY 180 QGDSGGLVNCQSLQGIISWGQDPCATIRKPGVYTKCKYVDWIQETMKN 230

Db 182 QGDSGGLVNCQSLQGIISWGQDPCATIRKPGVYTKCKYVDWIQETMKN 231

Search completed: December 23, 2002, 14:22:43
Job time : 51 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 23, 2002, 14:27:32 ; Search time 91 Seconds
(without alignments)
1003.047 Million cell updates/sec

Title: US-09-856-320a-2_COPY_53_282

Perfect score: 1263
Sequence: 1 RIIRGFECKRHSQPMQAAIF.....GYTYKCKYVWIOETKNN 230

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 713392

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPRO.spool/US09856320/runat_23122002_113713_22750/app.query.fasta_1.1391
-DB=Published.Applications.NA -OFMT=fastap -SUFFIX=rmpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=DIOSum62
-TRANS=human40.cdt -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09856320 -ECGN_1.1.49 -runat_23122002_113713_22750
-NCPU=6 -ICPU=3 -NO_XLPHY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WRT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published.Applications.NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCF_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCFUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	739	58.5	1375	10	US-09-764-898-68
2	719	56.9	924	10	US-09-764-898-140
3	719	56.9	924	10	US-09-764-847-253
4	684	54.2	963	10	US-09-888-615-31

5	683	54.1	999	9	US-09-978-295A-394	Sequence 394, App
6	683	54.1	999	9	US-09-978-697-394	Sequence 394, App
7	683	54.1	999	9	US-09-978-192A-394	Sequence 394, App
8	683	54.1	1343	10	US-09-796-294-72	Sequence 72, App1
9	683	54.1	1360	10	US-09-796-294-6	Sequence 6, App1
10	649.5	51.4	1381	10	US-09-739-907-52	Sequence 52, App1
11	649.5	51.4	1516	10	US-09-739-907-37	Sequence 37, App1
12	649.5	51.4	1570	9	US-09-992-598-308	Sequence 308, App
13	649.5	51.4	1570	9	US-09-989-293A-308	Sequence 308, App
14	649.5	51.4	1570	10	US-09-989-722-308	Sequence 308, App
15	649.5	51.4	1570	10	US-09-989-723-308	Sequence 308, App
16	649.5	51.4	1570	10	US-09-989-279-308	Sequence 308, App
17	649.5	51.4	1570	10	US-09-989-727-308	Sequence 308, App
18	649.5	51.4	1570	10	US-09-989-731-308	Sequence 308, App
19	649.5	51.4	1570	10	US-09-989-721-308	Sequence 308, App
20	649.5	51.4	1570	10	US-09-991-073-308	Sequence 308, App
21	649.5	51.4	1570	10	US-09-990-442-308	Sequence 308, App
22	649.5	51.4	1570	10	US-09-991-163-308	Sequence 308, App
23	649.5	51.4	1570	10	US-09-993-604-308	Sequence 308, App
24	649.5	51.4	1570	10	US-09-990-456-308	Sequence 308, App
25	649.5	50.4	1476	10	US-09-989-762-2	Sequence 2, App1
26	636.5	50.4	1476	10	US-09-764-762-2	Sequence 2, App1
27	577.5	45.7	1439	10	US-09-739-907-53	Sequence 53, App1
28	567	44.9	871	10	US-09-962-832-101	Sequence 101, App
29	567	44.9	871	10	US-09-880-107-2307	Sequence 2307, App
30	566.5	44.9	1678	10	US-09-925-300-153	Sequence 153, App
31	561	44.4	861	10	US-09-925-297-286	Sequence 286, App
32	556.5	44.1	3423	10	US-09-755-100-5	Sequence 5, App1
33	556.5	44.1	3846	10	US-09-755-100-3	Sequence 3, App1
34	556.5	44.1	4661	10	US-09-755-100-1	Sequence 1, App1
35	556.5	44.1	4661	10	US-09-755-100-2	Sequence 2, App1
36	554	43.9	945	10	US-09-728-952-16	Sequence 16, App1
37	549.5	43.5	1729	10	US-09-969-708-598	Sequence 598, App
38	548	43.4	969	10	US-09-888-615-39	Sequence 39, App1
39	548	43.4	969	10	US-09-818-243-30	Sequence 30, App1
40	548	43.4	969	10	US-09-905-083-30	Sequence 30, App1
41	532.5	42.2	765	9	US-10-012-896-524	Sequence 524, App
42	532.5	42.2	765	10	US-09-759-143-524	Sequence 524, App
43	532.5	42.2	765	10	US-09-780-669-524	Sequence 524, App
44	532.5	42.2	765	10	US-09-822-827-524	Sequence 524, App
45	531.5	42.1	1350	9	US-10-012-896-616	Sequence 616, App

ALIGNMENTS

RESULT 1
US-09-764-898-68
; Sequence 68, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 1375
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-898-68

Alignment Scores:

Pred. No.: 3.08e-67
Score: 739.00
Percent Similarity: 73.36%
Best Local Similarity: 58.08%
Query Match: 58.51%
DB: 10
Length: 1375
Matches: 133
Conservative: 35
Mismatch: 61
Indels: 0
Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x US-09-764-898-68 (1-1375)

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QY      1 ArgTllelelysglypneglucyslysprohisserserlinprotrglnalaaleuphe 20
      67 CGTGCATCGGGGCGGAGGAATGTGCGCCCACTCCAGACCTTGCGAGCGCGGCTCTTC 126
QY      21 GlnlysthrargyleucysglyalaThrleuilealProargtrpleuLeuThra 40
      127 CACCTTACTGCGCTCTCTGTGGGCGACCTCAGTACGTACGCTGGCTGTCCACAGCT 186
QY      41 AlahiscysleuylsProargtryleValHisleuylglnHisasnleuGlnLysglu 60
      187 GCCACAGCGCGGCAAGCGGTATTCGTGGTCCGCTTGAGAGCAACACCTGTGAATGG 246
QY      61 GluGllysglucglnthrargthraThrGlnSerPheProhissProgllyPheasn 80
      247 GAGGCTCCGAGCAGCTGTCCGGGTACGAGCTTCTTCCCGACCTGTGCTTCAACAG 306
QY      81 SerleuproasnlysaAspHisArgasnAspIleMetleuValylsMetalaSerProval 100
      307 GACCTCAGCCCAATGACCAATGATGACATCATCTGATCCGCTGCCAGGCGAGGCA 366
QY      101 SerlethrpralaValaArgProleuthrLeuSerSerArgcysValThrAlaGlyThr 120
      367 CGTCTGAGTCTGCTGTGTGCAAGCCCTCAACCTCAGCCAGACCTGTGTCTCCAGCATG 426
QY      121 SerCysleuileserglytyrpglyserThrSerSerProglneuarGleuprohissThr 140
      427 CAGTGTCTCATCTCAGGCTGGGGGCGGTGTCCAGCCCAAGGCGGTGTTCAGTACA 486
QY      141 LeuarGcysAlaasnlethrlelleleGlnHisGlnLysGlnLysasnAlaTyProgly 160
      487 CTGCAAGTCTCAATCCAGACATCTGAGAACAACTCTGCTCACTGGGATACCCGGC 546
QY      161 AsnlethrAspThrmetValcysAlaSerValGlnGlnlygllyLysAspSerCysGln 180
      547 CACATCTCGGACAGACATGCTGTGTGGGCGGCTGTGGAGGGGCGGAGGTTCTCTGCGAG 606
QY      181 GlysAspserglytyrProleuValcysAsnGlnSerleuGlnlylelleSerTrpgly 200
      607 GGTGACTCTGGGGGCGGCTGTGTGCAATGAACTTGGCAGGCGGTGTCTGGGGGT 666
QY      201 GlnAspProcysAlaIlethrArgLysProgllyValtyrThrLysValcysLysTyVal 220
      667 GGTGAGCGCTGTCCAGACCCCGCGCGCGAGTTCACACGCGTATGCCACTACCTT 726
QY      221 AspTrpIleGlnLuthrMetLysasn 229
      727 GACTGATCCAGAAATCATGAGAAC 753
Db

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RESULT 2

US-09-764-898-140

; Sequence 140, Application US/09764898

; Patent No. US2002090673A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PJ201

; CURRENT APPLICATION NUMBER: US/09/764,898

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 311

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 140

; LENGTH: 924

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-764-898-140

Alignment Scores:

Pred. No.: 2,03e-65 Length: 924

Score: 719.00 Matches: 131

Percent Similarity: 71.628 Conservative: 33

Best Local Similarity: 57.218 Mismatches: 65

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Query Match: 56.93% Indels: 0
DB: 10 Gaps: 0
US-09-856-320a-2_copy_53_282 (1-230) x US-09-764-898-140 (1-924)
QY      1 ArgTllelelysglypneglucyslysprohisserserlinprotrglnalaaleuphe 20
      56 CGTGCATCGGGGCGGAGGAATGTGCGCCCACTCCAGACCTTGCGAGCGCGGCTCTTC 115
QY      21 GlnlysthrargyleucysglyalaThrleuilealProargtrpleuLeuThra 40
      116 CACCTTACTGCGCTCTCTGTGGGCGACCTTATCAGTACCGCTGTGCTCAGAGCT 175
QY      41 AlahiscysleuylsProargtryleValHisleuylglnHisasnleuGlnLysglu 60
      176 GCCACAGCGCGGCAAGCGGTATTCGTGGTCCGCTTGAGAGCAACACCTGTGAATGG 235
QY      61 GluGllysglucglnthrargthraThrGlnSerPheProhissProgllyPheasn 80
      236 GAGGCTCCGAGCAGCTGTCCGGGTACGAGCTTCTTCCCGACCTGTGCTTCAACAG 295
QY      81 SerleuproasnlysaAspHisArgasnAspIleMetleuValylsMetalaSerProval 100
      296 GACCTCAGCCCAATGACCAATGATGACATCATCTGATCCGCTGCCAGGCGAGGCA 355
QY      101 SerlethrpralaValaArgProleuthrLeuSerSerArgcysValThrAlaGlyThr 120
      356 CGTCTGAGTCTGCTGTGTGCAAGCCCTCAACCTCAGCCAGACCTGTGTCTCCAGCATG 415
QY      121 SerCysleuileserglytyrpglyserThrSerSerProglneuarGleuprohissThr 140
      416 CAGTGTCTCATCTCAGGCTGGGGGCGGTGTCCAGCCCAAGGCGGTGTTCAGTACA 475
QY      141 LeuarGcysAlaasnlethrlelleleGlnHisGlnLysGlnLysasnAlaTyProgly 160
      476 CTGCAAGTCTCAATCCAGACATCTGAGAACAACTCTGCTCACTGGGATACCCGGC 535
QY      161 AsnlethrAspThrmetValcysAlaSerValGlnGlnlygllyLysAspSerCysGln 180
      536 CACATYTCGGACAGACATGCTGTGTGGGCGGCTGTGGAGGGGCGGAGGTTCTCTGCGAG 595
QY      181 GlysAspserglytyrProleuValcysAsnGlnSerleuGlnlylelleSerTrpgly 200
      596 GGTGACTCTGGGGGCGGCTGTGTGCAATGAACTTGGCAGGCGGTGTCTGGGGGT 655
QY      201 GlnAspProcysAlaIlethrArgLysProgllyValtyrThrLysValcysLysTyVal 220
      656 GGTGAGCGCTGTCCAGACCCCGCGCGCGAGTTCACACGCGTATGCCACTACCTT 715
QY      221 AspTrpIleGlnLuthrMetLysasn 229
      716 GACTGATCCAGAAATCATGAGAAC 742
Db

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RESULT 3

US-09-764-847-253

; Sequence 253, Application US/09764847

; Patent No. US20020132767A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PC009

; CURRENT APPLICATION NUMBER: US/09/764,847

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 2003

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 253

; LENGTH: 924

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-764-847-253

Alignment Scores:

Pred. No.: 2,03e-65 Length: 924
 Score: 719.00 Matches: 131
 Percent Similarity: 71.62% Conservative: 33
 Best local Similarity: 57.21% Mismatches: 65
 Query Match: 56.93% Indels: 0
 DB: 10 Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x US-09-764-847-253 (1-924)

QY 1 Argillelelysglypneglucyslyspromhisserglnprotrpglnalalaaleuphe 20
 Db 56 CGTGCACATCGGGCGAGGATGTCGCCCACTCCAGCCTTGCGAGCGCGCTCTTC 115
 QY 21 Glnuyltharaglyleucysglyalathrleuilealaproargtrpleuethrala 40
 Db 116 CACCTACTCGCTCTCTGCGGCGCACCTCATCACTGACCGCTGCTCTCACACT 175
 QY 41 Alahiscysleuysproargtrylevalhiscuylglnhlsanleuglnlysglu 60
 Db 176 GCCCACTGCGCAGACCGATATCTGTGGGTCGCTGGAGAGCACACCTTGGAATG 235
 QY 61 Glucllycysgluglnthrarargthralathrgluserpheprohisproglpheaasn 80
 Db 236 GAGGGTCGGAGCAGCTTTCGGGTTACGACTTCTTCCCACTGCTGCTTACAG 295
 QY 81 SerleuproasnlysaaphisargasnaspilleuethleuVallyMetalaSerproval 100
 Db 296 GACCTCAGCCGCAATGACACATGATGATCATGCTGATCCGCTGCCAGAGGCA 355
 QY 101 SerlethrrtrpalaValargProleuthrleuserserargysvalthAlaglythr 120
 Db 356 CGTGTACTCGCTGTGTCAGCCCTCAACTCAGCCAGACTGTGTCTCCCAAGCATG 415
 QY 121 SerCysleuileserglYtrpGlySerThrSerSerProglInleuArgleuprohisthr 140
 Db 416 CAGGTCTCATCTCAGGCTKGGGGGCGWRTCCAGCCCAAGGCGCTTTCAGTCA 475
 QY 141 LeuargCysalaasnlethrllelelughisglnlyscysgluasnAlaThrProglY 160
 Db 476 CTGAGTGTGCCAATCAGCATCTGAGAACTGTCACTGCGCATACCTGCGC 535
 QY 161 AsnlethrrtrpaleuValargCysalaserValglnlygllylsasSerCysgln 180
 Db 536 CACATTCGAGCAGCATGTCTGTGCGGCGCTGTGGGGGGCGCGGTTCTGCGAG 595
 QY 181 GlnaspserglYglYProleuValCysasnGlnserleuglnlylleleSerTrpGly 200
 Db 596 GGTACTTGTGGGGCGCCCTGTTTCCATGAACTTGGCAGCGGTGTCTGGGGGT 655
 QY 201 GlnaspProCysalailethrararglysproglyValtyrthrllyValCyslystYVal 220
 Db 656 GCTGARCCTGCTCCAGACCCCGCGCCGACGTTACACACGATATGCTACTT 715
 QY 221 AsptrpIleaglInglutInthMetlyAsn 229
 Db 716 GACTGGATCCAAAGATCATGTAGAGAAC 742

RESULT 4

US-09-888-615-31
 ; Sequence 31, Application US/09888615
 ; Patent No. US20020064856A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PLOMMAN, GREGORY
 ; APPLICANT: WHITE, DAVID
 ; APPLICANT: CAENEPEEL, SEAN
 ; APPLICANT: CHARITCZAK, GLEN
 ; APPLICANT: MANNING, GERRARD
 ; APPLICANT: SODARSANM, SUCHA
 ; TITLE OF INVENTION: NOVEL PROTEASES
 ; FILE REFERENCE: 038602/1214
 ; CURRENT APPLICATION NUMBER: US/09/888,615
 ; CURRENT FILING DATE: 2001-06-26
 ; PRIOR APPLICATION NUMBER: 60/214,047

; PRIOR FILING DATE: 2000-06-26
 ; NUMBER OF SEQ ID NOS: 150
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 31
 ; LENGTH: 963
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-888-615-31

Alignment Scores:

Pred. No.: 8.8e-62 Length: 963
 Score: 684.00 Matches: 124
 Percent Similarity: 67.08% Conservative: 37
 Best local Similarity: 51.67% Mismatches: 65
 Query Match: 54.16% Indels: 14
 DB: 10 Gaps: 3

US-09-856-320a-2_COPY_53_282 (1-230) x US-09-888-615-31 (1-963)

QY 1 Argillelelysglypneglucyslyspromhisserglnprotrpglnalalaaleuphe 20
 Db 253 AAGTTGCTGAAGGAGAGAGTGTGCACCCACATCCAGCATGGCAAGTGGCTCTAC 312
 QY 21 Glnuyltharaglyleucysglyalathrleuilealaproargtrpleuethrala 40
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RESULT 5

US-09-978-295A-394
 ; Sequence 394, Application US/09978295A
 ; Patent No. US20020156006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
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: PRIOR FILING DATE: 1998-05-15
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: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085573
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085704
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085697

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Alignment Scores: 1,18e-61 Length: 999
Pred. No.: 683.00 Matches: 116
Score: 70.678 Conserved: 43
Percent Similarity: 51.56% Mismatches: 64
Best Local Similarity: 54.08% Indels: 2
Query Match: 9 Gaps: 2

US-09-856-320a-2_COPY_53_282 (1-230) x US-09-978-295a-394 (1-999)

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QY 21 GlulysThrArgleuleucysglyAlaThrleulealaprodytprleuleThra 40
Db 319 CAGGCGCAGCACTACTCTGTGGGGGTCTCTGTAGGTGGCAACTGGGCTTACAGCT 378
QY 41 AlaHiscysleuysproargtyrileValHiscysleuglylnHiscysleuglyln 60
Db 379 GCCCAGCTGTAATAAACGAAATACACAGTACGCTGGAGACACACAGCTCAGAAATAA 438

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QY 61 GlulysCysgluInThrArgThrAlaThrGluSerPheProHISProGlyPheAsn 80
Db 439 GATGGCCAGAGCAAGAAATACCTGGTGGTTCATCCACACACCTGCTACACAGC 498
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Db 499 AGC---GATGTGGAGGACACACCATATCTGATGCTTCTTCACACTCGTGACCAGCA 555
QY 101 SerIleThrTrpAlaValArgProleuThrIleuSerSerArgCysValThrAlaGlyThr 120
Db 556 TCCTCGGGGTCCAAAGTAAGCCATCAGCTCGCAGATCAATGACACCAAGCTGCGCAG 615
QY 121 SerCysleuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHISThr 140
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QY 141 LeuArgCysAlaAsnIleThrIleIleGluHISGlnLysCysGluAsnAlaTrpProGly 160
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QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGln 180
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QY 221 AspTrpIleGlnGlu 225
Db 913 GACTGATCAGCAGAG 927

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RESULT 6
US-09-978-697-394
Sequence 394, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:

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: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Bolstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630P1C27
: CURRENT APPLICATION NUMBER: US/09/978,697
: CURRENT FILING DATE: 2001-10-16

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Score: 683.00 Matches: 116
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Query Match: 54.08% Indels: 2
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DB 853 TCAG1ACC1CG1TGG1G1AG1TCC1GAC1AA1C1G1G1G1CT1AT1AC1CA1A1CT1G1CG1TAC1CTG 912

QY 221 Asp1TTP1le1G1n1G1u 225
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RESULT 7
US-09-978-192A-394
Sequence 394, Application US/09978192A
Patent No. US2002017553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
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Qy	21	GLIYSTRARGLLEULEUCYSGLYALATHLEULEIALAARPRGRYTRPLEULEUTHRALA	40
Db	319	CAGGGCCAGCAACACTCTCTGGGGGGGTGTCCTTGTAGGTGGCAACGTGGTGCTTACAGCT	378
Qy	41	ALAHISCSYLEULYSProARGYTRILEVALHISLEUGLYGLNHISAsnLEUGLINTYSGLU	60
Db	379	GCCCACTGTATAAAAAACGGAATATNACAGTACGCTGGGAGAACCAAGCCCTNCAAGATMAA	438
Qy	61	GLIUGLYCSGLIUGLINTHRAryTHRALArthGLUSERPheProHISProGLIYpHeasAsn	80
Db	439	GATGGCCCAAGCAAGAAATACCTGTGTGTTCAAGTCCATCCCAACCCCTCTCAACAGC	498
Qy	81	SerLEUProAsnLYSAspHISArgAsnAspLEUleUleValLYSMeTAlAserProVAL	100
Db	499	AGC---GATGTGGAGAGCACCAACCATGATGTGATGTCTTCAACTGCGCTGACCAAGCA	555
Qy	101	SerLEUThrTRPALAVALArgProLEUThrLEUSERSerArgCYSVALThrAlaGLYThr	120
Db	556	TCCCTGGGGGTCCAAAGTAGAAGCCCATGAGCCTGGCAGATCATTTGCAACCCAGCCTGGCAG	615
Qy	121	SerCYSLeuLIESerGLYTRPGLYSerThrSereSerProGLINLeuArgLEUProHISThr	140
Db	616	AAGTGCACCCGCTCAGGTGGGGGACGTGCACACGATCCCGAGAGAAATTTCTGTGACACT	675
Qy	141	LeuArgCYSAlaAsnLIEthRIleLEGLNHISGLINYSCSGLuAsnAlaTYRProGLY	160
Db	676	CTCAACTGTGCAGAGATRAAAATTTTCCCCAGAGAAGTGTGAGCATGCTTACCCGGGG	735
Qy	161	AsnLIEthraspThrMetValCYSAlaSerValGLINGLUGLYGLYAspSereCYSGLN	180
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Qy	181	GLYAspSereGLYGLYProLEUValCYSAsnGLINserLEUGLINTYGLIIESerTPGLY	200
Db	793	GCCCACTGTGAGAGCCCCCTGGTGTGTGATGTGTGCTCACTCCAGGGCATCACATCTGGGGC	852
Qy	201	GLINAspProCYSAlaLIEthRAryLysProGLYValTYRThrLYSValCYSLYSTYVal	220
Db	853	TCAGAGCCCTGTGGAGAGTGCAGCAACCTGGCGTATATACCAACATCTGCCCTACCTG	912
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: GENERAL INFORMATION:			
: APPLICANT: O'Brien, Timothy J.			
: TITLE OF INVENTION: Extracellular Serine Protease			
: FILE REFERENCE: D6020CIP3			
: CURRENT APPLICATION NUMBER: US/09/796,294			
: CURRENT FILING DATE: 2001-02-28			
: PRIOR APPLICATION NUMBER: US 09/618,259			
: NUMBER OF SEQ ID NOS: 72			
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: FEATURE:			
: OTHER INFORMATION: Anti-sense sequence of TADG-14			
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QY 21	GlulysThrArgleuleuCySgLYAlaThrleuilealaproArgTrpleuleuThrAla	40		
DB 675	CAGGGCCGACCAACTCTGTGGCGGTCTCTGTAGCTGGCAACTGGGCTTCACAGCT	616		
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DB 615	GCCCACTTAAATAAAGCAATATACACAGTACGCTGGGAGAACCCACACCTACAGAAATAAA	556		
QY 61	GlulGlyCysGlulInThrArgThrAlaThrGluSerPheProhissProGlyPheasnasn	80		
DB 555	GATGGCCCAAGCAAGAAATACCTGTGTGTCATGACATCCACACCCCTGTACAAAG	496		
QY 81	SerLeuProasnLysAspHisArgAsnAspLleMetLeuValLysMetAlaSerProval	100		
DB 495	AGC---GATGTGGAGGACACCAACCAATGATCTGATGCTTCTCAACGCGTCGACCAAGCA	439		
QY 101	SerIleThrTrpAlaValArgProleuThrLeuSerSerArgCysValThrAlaGlyThr	120		
DB 438	TCCCTGGGGTCCAAAGTAACACCCATACAGCTGTGCACATATATTCACACCCAGCTGGCAG	379		
QY 121	SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProhissThr	140		
DB 378	AAGTCACACCTCTGAGGTGGGGGACACTGTACACAGTCCCGAGGAATTTCTCTGACACT	319		
QY 141	LeuArgCysAlaAsnIleThrLleLleGluHisIleLysCysGluAsnAlaTyrrProGly	160		
DB 318	CTCAACTGTGCAGAAAGTAATAAATTTTCCCCAGAAAGAGTGTGGATGCTTACCCGGGG	259		
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DB 201	GCGCATTTCTGAGGCCCTCTGTGTGTGATGTGTGCTCACTCCAGGGCACCACATCTGGGGC	142		
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QY 221	AspTrpIleGlnGlu	225		
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RESULT 9				
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Sequence 6, Application US/09796294				
Patent No. US20020037581A1				
GENERAL INFORMATION:				
APPLICANT: O'Brien, Timothy J.				
APPLICANT: Underwood, Lowell J.				
TITLE OF INVENTION: Extracellular Serine Protease				
FILE REFERENCE: D6020C1P3				
CURRENT APPLICATION NUMBER: US/09/796,294				
CURRENT FILING DATE: 2001-02-28				
PRIOR APPLICATION NUMBER: US 09/618,259				
PRIOR FILING DATE: 2000-07-18				
NUMBER OF SEQ ID NOS: 72				
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LENGTH: 1360				
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FEATURE:				

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# Prior FILLING DATE: 1998-07-09

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Percent Similarity: 68.10%    Conservative: 40
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DB: 9                  Gaps: 4

US-09-856-320A-2_COPY_53_282 (1-230) x US-09-989-293A-308 (1-1570)

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Db CGCATTCATCATGGATCGGATCGGATGCACACCAGCCGCTGCCGGCGGCTGTGG 608

QY 20 PhegluysThrArgleuleuLeySGlyAlaThrleuLeilaIparProatgTrrpleuLeuthr 39
Db CTAGAGGCCAACCAAGCTCTACTGCGGGGGCGGTGTGGTGCGATGCACAGTGGCTGTACG 668

QY 40 AlaAlahistyleuLysProatgTrrtleValnHlsleuglGlnHisAsnleuGlnLys 59
Db GCCGCCACATGCAGAGAAGAAAGTTTCAGATGCGCTCGGCCACATGCTACCTCCCTGCACA 728

QY 60 ---GlulugluCySgIuGlnInThArgThAlaThrcLusleuRhePrronHisProglyPhe 78
Db GTTTATGATCTGGGcAGcAGATGTTTCCAGGGGGCTCAAATCCATCCCCCAGCTGGCTGA 788

QY 79 AsnaIsnerleuproAdnlvASpBnIsArGaDnsApriIlemetleuVallysMetAlaser 98

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Db 789 TCC-----CACCCTGGCCACCTCTAACGACCTCATCTCAACTGAACAGA 836
Qy 99 ProValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAla 118
Db 837 AGAATCTCTCCACCTAAAGATGTCCAGACCCATCAACGCTCTCTCATGTCCCTCTCT 896
Qy 119 G1yThrSerCysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuPro 138
Db 897 GGGCAAAAGTCTGTGTCTGGCTGGGGGACCAACAGAGCCCAAGTCACTTCCCT 956
Qy 139 HisThrLeuArgCysAlaAsnIleThrIleIleGluHisGlnIysCysGluAsnAlaTyr 158
Db 957 AAGTCTCCACGCTCGAATATCATCAGCGTCACTGAGAAAAGTGGAGATCTCTTAC 1016
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Db 1017 CCGAGACAGATAGATGACACCATGTCTGCCCCGT---GACAAAGCAGTAGACACTCC 1073
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; Sequence 308, Application us/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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RESULT 15
US-09-989-723-308
Sequence 308, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavich, Ivay J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C62
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US/09/989,723
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; PRIOR FILING DATE: 1998-07-09

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Score: 649.50 Matches: 118
Percent Similarity: 68.108 Conservative: 40
Best Local Similarity: 50.868 Mismatches: 67
Query Match: 51.438 Indels: 7
DB: 10 Gaps: 4

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US-09-856-320A-2_COPY_53_282 (1-230) x US-09-989-723-308 (1-1570)

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

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(without alignments)
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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3	1263	100.0	1186	ABK92131	Prostate cancer-as
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6	1263	100.0	1204	AA521496	Human cDNA sequenc
7	1263	100.0	1204	AA54320	DNA encoding prote
8	1263	100.0	1204	ABL95664	Human angiogenesis
9	1263	100.0	1204	ABL88175	Human PRO1279 CDNA
10	1263	100.0	1292	ABK33628	CDNA encoding huma
11	1263	100.0	1301	ABK33732	Human secreted pro
12	1263	100.0	1301	AA61763	CDNA encoding huma
13	1263	100.0	1146	AA230222	CDNA encoding a hu
14	1253	99.2	1146	AAV84589	Human secreted pro
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18	1233	97.6	1191	AAK97777	Extended human sec
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20	1221.5	96.7	1052	AAK8798	Activation constru
21	1221.5	96.7	1052	AAK5270	Nucleotide sequenc
22	1218	96.4	833	AAV42925	DNA encoding a hum
23	1067	84.5	1323	AAV61764	CDNA encoding mous
24	916.5	72.6	618	ABK30233	Human G-protein-co
25	834	66.0	762	AAH31050	Human colon cancer
26	834	66.0	762	AAH31061	Human cDNA encodin
27	739	58.5	1375	AA526876	CDNA encoding nove
28	737	58.4	1365	AA541087	CDNA encoding nove
29	719	56.9	924	AA541622	CDNA encoding nove
30	719	56.9	924	AA526948	Human cDNA encodin
31	719	56.9	924	ABK41855	CDNA encoding nove
32	686	54.3	1322	AAK19534	Mouse ischaemic co
33	686	54.3	1333	AAK48519	Human neuropsin-en
34	686	54.3	1333	AAK63251	Mouse neuropsin ge
35	684	54.2	963	AAK30570	Human protease, pr
36	684	54.2	963	ABK31774	DNA encoding novel
37	684	54.2	1278	ABK48347	DNA encoding novel
38	683	54.1	809	AA587560	DNA encoding novel
39	683	54.1	868	AA244182	Human neuropsin cd
40	683	54.1	905	AA211029	Human serine prote
41	683	54.1	942	AAZ11030	Human serine prote
42	683	54.1	944	AAV84052	Nucleic acid encod
43	683	54.1	999	AAZ34225	Human PRO322 nucle
44	683	54.1	999	AAK78556	Human PRO322 (UNQ2
45	683	54.1	999	AA521441	Human cDNA sequenc

ALIGNMENTS

RESULT 1
AA222638
ID AA22638 standard; cDNA; 1106 BP.
XX
AC AA22638;
XX
AC
XX
DT 08-DEC-1999 (first entry)
XX
DE CASB12 nucleotide sequence.
XX
KW neuropsin; cancer; assay; inhibitor; serine protease; immunogenic;
KW ds.
XX
OS Homo sapiens.
XX
FH Key 14..862 location/Qualifiers
FT CDS /*tag= a

FT
XX
PN
XX
PD
XX
XX
PE
XX
PR
XX
PA
XX
PI
XX
DR
XX
PT
XX
PS

/product= CASH12

WO9949055-A1.

30-SEP-1999.

17-MAR-1999; 99WO-EP01894.

20-MAR-1998; 98GB-0006095.

(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

Bruck CEM, Cassart J, Coche T, Vinals-Bassols C;
WPI; 1999-580450/49.
P-PsDB; AAY42439.

New human serine protease CASH12, for treatment, prevention and diagnosis of cancer and autoimmune diseases -
Claim 10; Page 47; 58pp; English.

This is the nucleotide sequence of the CASB2 gene. The nucleotide sequence of AA222638 shows homology with neuropilin and the encoded protein AAY4439 is structurally related to other proteins of the serine protease family, having homology and/or structural similarity with neuropilin. It is expected that as well as similar structure, these proteins will also share similar biological functions and properties. The CASB2 polypeptides and polynucleotides can be used to develop methods for identifying agonists and antagonists/inhibitors of these molecules, and thereby treating conditions associated with CASB2 polypeptide imbalance. The invention also provides for diagnostic assays for detecting diseases associated with inappropriate CASB2 polypeptide activity or levels.

Since CASB2 is either specifically expressed or highly over-expressed in tumors compared to normal cells, the polypeptides and polynucleotides of the invention are believed to be important immunogens for specific prophylactic or therapeutic immunization against tumors. The polypeptides and polynucleotides can therefore be targeted by antigen specific immune reactions (which result in the destruction of the tumor cell) or they can be used to diagnose the occurrence of tumor cells.

Sequence 1106 BP: 247 A; 348 C; 287 G; 224 T; 0 other;

Alignment Scores:		
Pred. No.:	1.64e-105	1106
Score:	1263.00	230
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	20	Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x AA222638 (1-1106)

OY	1	ArgIleIleLVySGlyPheGLiCysLVyProHiseSerGlnProTyrGlnAlaIlePhe	20
Db	170	AGGATCATCAAGGGTTTGATGATGCAAGCTACTCTCCAGACCTTGGACGACGCCCTGTTC	2299
OY	21	GluLVyThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTyrLeuLeuThrAla	40
Db	230	GAGAGAGACGGCGGTACTCTGTGGGGCGACGGCTCATGCCGCCCAAGATGGCTCTGACAGCA	289
OY	41	AlaHIScysLeuLVyProArgTyrLlIleAlHISleuGLiGlnHISAsnLeuGlnLVyGlu	60
Db	290	GCCCACTGCTCAAGCCCCGGCTACATATGTTTACCTGGGGCAGCAACCTTCCAGAAAGAG	349
OY	61	GluGLiCysGluGlnIleThrArgThrAlaThrGluSerPheProHISProGluPheAsn	80
Db	350	GAGGCGTGTGAGCAGACCCCGACAGCCACTGATGTCCTTCCGCCACCCGGGCTTCAACAC	409
OY	81	SerLeuProAsnLVyAspPheIleArgAsnAspLlIleMetIleValLVyMetAlaSerProVal	100
Db	410	AGCTTCCCAACAAAGACCAACCGCAATGACTCTATGCTGGGAAGATGGATGGCCAGTC	469

QY	101	serIlethrppalaValaIrgProleuthrIeusSerargCysValThrIalagIYth	120
Db	470	TCcATcACcCTGGGCGTgTCgACACCCCTcACCTCTCTCTCAGCGTGTCTcACTGCTGGcACC	529
QY	121	SerCysIleuIleSerGIYTrpGIYSerThrSerSerProGlnIleuAgluProHIsThr	140
Db	530	AGCTcGCTcATTTCCGGGTGGGGAGcACGTCcAGCCcCCcAGTTAGcCTGTGGCTcACAC	589
QY	141	IleuArgCysAlaAsnIleThrIleIleGlnHIsGlnIYcSGIuSnaIaIYTrpGly	160
Db	590	TTTGcATTCGGcGcCAACATcACcATcATTGAGcACcAGAAgTGTGAAGcGCTcACCCcGGc	649
QY	161	AsnIleThrAspThrMetValCysAlaSerValGlnIuGlnIYgIYLYsaSPSerCysGln	180
Db	650	AACATcACAGAcACcACCATGTGTGTGCCAGcCTGcAGGAAGGGGGcCAAGAcCTCTGGcAG	709
QY	181	GlyAspSerGIYgIYProIeuValCysAsnGlnSerIeuGlnIYIleIleSerTrpGIY	200
Db	710	GATGTACTCCGGGGGGcCTCTGTGTGTATACcAGTCTCTTCAGGcCATTTACTCTCTGGGGc	769
QY	201	GlnAspProCysAlaIleThrArgLYsProGlyAlYThrIYrIYsValCysLYsTrYVal	220
Db	770	CAGGATCCGTGTGGcATcACCCGAAAcCTGTGTCTTACcAGAAgTGTGCcAAATATGTG	829
QY	221	AspTrpIleGlnIuThrMetLYsAsnAsn	230
Db	830	GACTGTGATCCAGAcAGAcATGATAAcACAT	859

RESULT 2
AAZ22639
ID AAZ22639 standard; cDNA; 1158 BP

DT 08-DEC-1999 (first entry)

CASB12 derived from Expressed Sequence Tag sequences.

KW neuropsin; cancer; assay; inhibitor; serine protease; immunogenic;
KW autoimmune disease; ds.

OS Homo sapiens.

FH	key	Location/Qualifiers
1	1	1
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3	3	3
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5	5	5
6	6	6
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99	99	99
100	100	100

```

FT      /*tag= a
FT      /product= CASB12

```

PN W09949055-A1.

PD 30-SEP-1999.

PE 17-MAR-1999; 99WO-EP01894.

PR 20-MAR-1998; 98GB-0006095.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Bruck CEM, Cassart J, Coche T, Vinals-bassols C; ...

DR WPI; 1999-580450/49.

XX

PT diagnosis of cancer and autoimmune diseases -

PS Claim 26; Page 49; 58pp; English.

CC This is the nucleotide sequence of the CASB12 gene derived from
CC Expressed Sequence Tag (EST) search for tumor-specific and
CC tumor-associated antigens. The nucleotide sequence of AA222658 shows
CC homology with neuropsin and the encoded protein ANV2439 is structurally

CC related to other proteins of the serine protease family, having homology
 CC and/or structural similarity with neuropilin. It is expected that as well
 CC as similar structure, these proteins will also share similar biological
 CC functions and properties.
 CC The CASB12 polypeptides and polynucleotides can be used to develop
 CC methods for identifying agonists and antagonists/inhibitors of these
 CC molecules, and thereby treating conditions associated with CASB12
 CC polypeptide imbalance. The invention also provides for diagnostic assays
 CC for detecting diseases associated with inappropriate CASB12 polypeptide
 CC activity or levels.
 CC Since CASB12 is either specifically expressed or highly over-expressed
 CC in tumors compared to normal cells, the polypeptides and polynucleotides
 CC of the invention are believed to be important immunogens for specific
 CC prophylactic or therapeutic immunization against tumors. The
 CC polypeptides and polynucleotides can therefore be targeted by antigen
 CC specific immune reactions (which result in the destruction of the tumor
 CC cell) or they can be used to diagnose the occurrence of tumor cells
 CC
 SQ Sequence 1158 BP; 274 A; 359 C; 306 G; 219 T; 0 other;

Alignment Scores:
 Pred. No.: 1,73e-105 Length: 1158
 Score: 1263.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x AA22639 (1-1158)

QY 1 ArgIleIleIySgIyPheGluCysLysProHisSerGlnProTrpGlnAlaIleuPhe 20
 Db 240 AGGATCATCAAGCGGTGAGTGCACAGCCACCTCCAGCCCTGGCAGGCGCTGTTC 299
 QY 21 GluIySthArgLeuLeuCysGlyAlaThrIleuIlealProaGtYrPleuIleuThAla 40
 Db 300 GAGAAAGCGGCTACTCTGTGGGGGCAAGCTCAAGCCCAAGATGGCTCTTACAGCA 359
 QY 41 AlaHisCysLeuIySProaGtYrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
 Db 360 GCCCAGTCCCTCAAGCCCGCTACATGATTACCTGGGGGCAACAACCTCCAGAAAGAG 419
 QY 61 GluIyGysGluGlnIhTrArgThAlaThrGluSerPheProHisProGlyPheAsnAsn 80
 Db 420 GAGGGCTGTGAGCAGCCCGGACAGCCACGACGTCCTTCCCGCCCGGCTTCAACAAC 479
 QY 81 SerLeuProaSnIySAsPHisArgAsnAsPleuMetLeuValIySMetAlaSerProVal 100
 Db 480 AGCTCCCAAGAAAGACACCGCATGACATCTGCTGTGAAAGATGGCTCCAGTC 539
 QY 101 SerIleThrTrpAlaValArgProLeuThrLeuSerArgCysValIhAlaGlyThr 120
 Db 540 TCCATACACGTGGGCTGTGGCAGCCCTCACCTCCCTCAAGCTGTGACGTGGCAGC 599
 QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
 Db 600 AGCTGCTCATTTCCGCTGGGGGACAGCAGTCCAGCCCGCAGTTACCCCTGCTCACACC 659
 QY 141 LeuArgCysAlaAsnIleThrIleIleGluHisGlnIySgIyuaAnaIATYrProGly 160
 Db 660 TTGGGATGGCCCAACATCATCATATTGAGCAGCAAGAGTGTGAAGCGCTTACCCGGC 719
 QY 161 AsnIleThrAspIhMetValCysAlaSerValGlnGluGlyIyLysAspSerCysGln 180
 Db 720 AACATCAGACAGACCATGTGTGTGCCAGGTCAGAGAAGGGGGCAAGGACTCTGGCAG 779
 QY 181 GlyAspSerGlyIyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 200
 Db 780 GGTGACTCCGGGGGCGCTGTGTGTACACAGCTCTTCAAGCATTAATCTCTGGGGC 839
 QY 201 GlnAspProCysAlaIleThrArgLysProGlyValIyThrIyLysValCysLysTyVal 220
 Db 840 CAGGATCCGTGTGTGATCACCAGCAAGCCTGTGTCTACAGAAAGTCTGCAATATATGTG 899

QY 221 AspTrpIleGlnIyThrMetLysAsnAsn 230
 Db 900 GACTGATCCAGAGACGATGACAGACAT 929

RESULT 3

ID ABR92131 standard; DNA; 1186 BP.

XX ABR92131;

DT 15-AUG-2002 (first entry)

XX Prostate cancer-associated DNA sequence #17.

KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
 gene therapy; gene; ds.

XX Mammalia.

PN WO200230268-A2.

PD 18-APR-2002.*

PF 12-OCT-2001; 2001WO-US32045.

PR 13-OCT-2000; 2000US-0687576.

PR 08-DEC-2000; 2000US-0733288.

PR 08-DEC-2000; 2000US-0733742.

PR 24-JAN-2001; 2001US-263957P.

PR 16-MAR-2001; 2001US-276791P.

PR 06-APR-2001; 2001US-281922P.

PR 24-APR-2001; 2001US-286214P.

PR 30-APR-2001; 2001US-0847046.

PR 04-MAY-2001; 2001US-288589P.

PA (BOSB-) BOS BIOTECHNOLOGY INC.

PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezl P;

DR WPI; 2002-471335/50.

XX P-PSDB; ABG61816.

PT Detecting a prostate cancer-associated transcript in a cell in a

PT patient, useful for diagnosing prostate cancer (PC) or screening

PT modulators of PC, by determining if prostate cancer-associated genes

XX are expressed in a prostate tissue

XX Claim 22; Page 313; 436pp; English.

CC The present invention relates to methods of detecting a prostate

CC cancer-associated transcript in a cell from a patient. The method

CC comprises contacting a biological sample from the patient with

CC prostate cancer-associated polynucleotides (designated PC genes) that

CC selectively hybridize to a sequence that is at least 80% identical

CC to them. The prostate cancer-associated polynucleotide sequences

CC are differentially expressed in prostate tumour tissue or in

CC prostate cancer and are derived from the tissues of various

CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).

CC The methods of the invention are useful for diagnosing and treating

CC prostate cancer in mammals. The prostate cancer-associated genes are

CC useful for diagnosing or treating prostate cancer, as well as for

CC identifying modulators of prostate cancer or agents that inhibit

CC prostate cancer. The nucleic acid sequences are particularly useful

CC in gene therapy, as a vaccine or in antisense applications.

CC ABR92115-ABR92263 represent prostate cancer-associated polynucleotide

CC sequences.

SQ Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 other;

Alignment Scores: 1.79e-105 Length: 1186

PR	16-SEP-1996;	9805-0100627
PR	16-SEP-1996;	9805-0100661
PR	16-SEP-1996;	9805-0100662
PR	16-SEP-1996;	9805-0100664
PR	17-SEP-1996;	9805-0100683
PR	17-SEP-1996;	9805-0100684
PR	17-SEP-1996;	9805-0100710
PR	17-SEP-1996;	9805-0100711
PR	17-SEP-1996;	9805-0100930
PR	17-SEP-1996;	9805-0100939
PR	17-SEP-1996;	9805-0100930
PR	18-SEP-1996;	9805-0100848
PR	18-SEP-1996;	9805-0100849
PR	18-SEP-1996;	9805-0101014
PR	18-SEP-1996;	9805-0101068
PR	18-SEP-1996;	9805-0101071
PR	22-SEP-1996;	9805-0101379
PR	23-SEP-1996;	9805-0101471
PR	23-SEP-1996;	9805-0101472
PR	23-SEP-1996;	9805-0101475
PR	23-SEP-1996;	9805-0101476
PR	23-SEP-1996;	9805-0101477
PR	23-SEP-1996;	9805-0101478
PR	24-SEP-1996;	9805-0101738
PR	24-SEP-1996;	9805-0101741
PR	24-SEP-1996;	9805-0101743
PR	24-SEP-1996;	9805-0101915
PR	24-SEP-1996;	9805-0101916
PR	29-SEP-1996;	9805-0102207
PR	29-SEP-1996;	9805-0102240
PR	29-SEP-1996;	9805-0102307
PR	29-SEP-1996;	9805-0102307
PR	29-SEP-1996;	9805-0102330
PR	29-SEP-1996;	9805-0102331
PR	30-SEP-1996;	9805-0102484
PR	30-SEP-1996;	9805-0102487
PR	30-SEP-1996;	9805-0102570
PR	30-SEP-1996;	9805-0102571
PR	01-OCT-1996;	9805-0102684
PR	01-OCT-1996;	9805-0102687
PR	02-OCT-1996;	9805-0102965
PR	06-OCT-1996;	9805-0103458
PR	07-OCT-1996;	9805-0103315
PR	07-OCT-1996;	9805-0103315
PR	07-OCT-1996;	9805-0103328
PR	07-OCT-1996;	9805-0103395
PR	07-OCT-1996;	9805-0103396
PR	08-OCT-1996;	9805-0103401
PR	08-OCT-1996;	9805-0103633
PR	08-OCT-1996;	9805-0103679
PR	08-OCT-1996;	9805-0103711
PR	14-OCT-1996;	9805-0104257
PR	20-OCT-1996;	9805-0104987
PR	20-OCT-1996;	9805-0105000
PR	20-OCT-1996;	9805-0105002
PR	21-OCT-1996;	9805-0105104
PR	22-OCT-1996;	9805-0105169
PR	22-OCT-1996;	9805-0105266
PR	26-OCT-1996;	9805-0105593
PR	26-OCT-1996;	9805-0105594
PR	27-OCT-1996;	9805-0105807
PR	27-OCT-1996;	9805-0105811
PR	27-OCT-1996;	9805-0105862
PR	27-OCT-1996;	9805-0106062
PR	28-OCT-1996;	9805-0106023
PR	28-OCT-1996;	9805-0106029
PR	28-OCT-1996;	9805-0106030
PR	28-OCT-1996;	9805-0106033
PR	28-OCT-1996;	9805-0106178
PR	29-OCT-1996;	9805-0106248
PR	29-OCT-1996;	9805-0106584

PR 29-OCT-1998; 98US-0108500.
PR 30-OCT-1998; 98US-0106464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 03-NOV-1998; 98US-0106934.
PR 10-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108775.
PR 17-NOV-1998; 98US-0108779.
PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.
PR 17-NOV-1998; 98US-0108801.
PR 17-NOV-1998; 98US-0108802.
PR 17-NOV-1998; 98US-0108806.
PR 17-NOV-1998; 98US-0108807.
PR 17-NOV-1998; 98US-0108867.
PR 18-NOV-1998; 98US-0108925.
PR 18-NOV-1998; 98US-0108848.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108858.
PR 18-NOV-1998; 98US-0108904.
XX (GETH) GENENTECH INC.
XX
PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT.
XX WPI, 2000-237871/20.
XX P-PSDB; AAY99390.
XX
PT New mammalian DNA sequences encoding transmembrane, receptor or
PT secreted PRO polypeptides, useful for screening of potential peptide or
PT small molecule inhibitors of the relevant receptor/ligand interactions
XX
XX Claim 2; Fig 101; 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
XX receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
XX transmembrane and receptor PRO proteins can be used for screening of
XX potential peptide or small molecule inhibitors of the relevant
XX receptor/ligand interactions. The polypeptides and nucleotide sequences
XX encoding them have various industrial applications, including uses as
XX pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
XX PCR primers and hybridisation probes used in the isolation of the PRO
XX polypeptides from the present invention.
SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:
Pred. No.: 1,82e-105 Length: 1204
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-856-320a-2_copy_53_282 (1-230) x AAA37072 (1-1204)
QY 1 ArgIleIleIleSgIlypHeGlyucLySProHISserGlnProTrpGlnAlaIleAlaLeupHe 20
DB 166 AGGATCATCAAGGGGTTCGAGTCGACGACCTCCAGCCCTGGGAGGAGCCCGTTC 225
QY 21 GluLySThrArgIleuLeuSgIlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 40
DB 226 GAAACAACCGCGCTACTCTGTGGGGGAGCGCTCATCGCCCGGAGATGCTCCGACAGCA 285
QY 41 AlaHisCysLeuLysProArgTrpIleValIleHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
DB 286 GCCCATCTGCTCAAGCCCGCTCATATGTTACCTGGGGGAGCACAACCTCCGAGAGGAG 345

QY 61 GluGlyCysGlnGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsn 80
DB 346 GAGGGCTGTGAGCAGACCCGAGACAGCCATGAGTCTTCCGCCACCCGGCTTCACAAAC 405
QY 81 SerLeuProAsnLysAspHisIleArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
DB 406 AGCCTCCCAACAAAGCCACCCCAAGACATCATGTGTGTGAAGTGGCATGCGCAGTTC 465
QY 101 SerIleThrTrpAlaValAlaGProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
DB 466 TCCATCACTCTGGGCTGTGGCACCCTTCACCTCTCTCCACGCTGTGTCACTGTGGCACC 525
QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
DB 526 AGCTGCTCATTTCCGGCTGGGAGACAGCTCCAGCCCGCCAGTTAGGCTTCACACAC 585
QY 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaIleTrpGly 160
DB 586 TTGCGATGCCCAACATCACCATCATTTGACACACAGAGTGTGAGAACCGCTACCCCGGC 645
QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
DB 646 AACATCAACACACCATGTTGTGTCCAGCGCTCAGAGAGGGGCGAAGACTCTCCGAC 705
QY 181 GlyAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 200
DB 706 GGTGACTCCGGGGGCCCTGTGTCTGTAAACACAGTCTTCAAGCATTTATCTCTGGGGC 765
QY 201 GlnAspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpVal 220
DB 766 GAGGATCCGTTGTCGATCACCCGAAAGCCGTGTCTACACGAAAGTCTGCAATATG 825
QY 221 AspTrpIleGlnGlnIleThrMetLysAsnAsn 230
DB 826 GACTGATCCAGAGACGATGAGAAACAAT 855

RESULT 6
ID AAS21496
XX AAS21496 standard; cDNA; 1204 BP.
AC AAS21496;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human cDNA sequence encoding for PRO1279 polypeptide.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.
XX
OS Homo sapiens.
XX
XX
XX WO200140466-A2.
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000MO-US32678.
XX
XX 01-DEC-1999; 99MO-US28301.
PR 01-DEC-1999; 99MO-US28634.
PR 02-DEC-1999; 99MO-US28551.
PR 02-DEC-1999; 99MO-US28564.
PR 02-DEC-1999; 99MO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99MO-US30095.
PR 20-DEC-1999; 99MO-US30911.
PR 20-DEC-1999; 99MO-US30999.
PR 30-DEC-1999; 99MO-US31243.
PR 06-JAN-2000; 2000MO-US00277.
PR 06-JAN-2000; 2000MO-US00376.
PR 11-FEB-2000; 2000MO-US03565.

PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07332.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 XX
 PA (GETH) GENENTECH INC.
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
 PI Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI: 2001-408281/43.
 DR P-PSDB; AAU12424.
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical .
 PS Claim 3; Fig 505; 813pp; English.
 XX
 CC AA52144-AA521518 encode for novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIa. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX
 SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
 Alignment Scores:
 Pred. No.: 1.82e-105 Length: 1204
 Score: 1263.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-09-856-320a-2_COPY_53_282 (1-230) x AA521496 (1-1204)
 QY 1 ArgilleleuysglyphneglucysylsProhisserginProtrpGlnAlaAlaLeuPhe 20
 Db 166 AGATCATCAAGGGGTGAGTGCAGAGCTACCTCCAGCCCTGCGAGGAGCCCTGTTG 225
 QY 21 GllulsthratgLeuLeuCySgilyAlaThrleuileAlaProargTyrPleuLeuThrAla 40
 Db 226 GAGAAAGACGGCGCTACCTGTGGGGCGACGCTATCGCCCAAGATGGCTCTGACAGCA 285
 QY 41 AlahiscysleuysProatgTyrIleValHisleuGlyGlnHisAsnLeuGlnlySglu 60

Db 286 GCCCACTGCCTCAAGCCCCCGCTACATAGTCACTGGGGGAGACAACTCCAGAAAGAG 345
 QY 61 GlulglycysgluglnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsn 80
 Db 346 GAGGGCTGTGAGCAGACCCGGAGACCCAGCTAGTCTCTTCCCCAGCCGGCTTCAACAC 405
 QY 81 SerleuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
 Db 406 AGCGTCCCAACAAAGACACACCGCAATGACATCATCGTGGTGAAGATGGATCCGCACTC 465
 QY 101 SerIleThrTrpAlaValArgProLeuThrIleuSerSerArgCysValThrAlaGlyThr 120
 Db 466 TCCATCACCCTGGGTGTGCGACCCCTCACCTCTCCACCTGTGTCACTGTGGCACC 525
 QY 121 SerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
 Db 526 AGCTGCCCTCATTTTCCGGGTGGGGGAGCAGCTCCAGCCCCCGATTACGCTTCCACMC 585
 QY 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGly 160
 Db 586 TTGGCATCGCCCAACATCACCATCATTTGAGCAGCAGAAAGTGTGAAGACGCTACCCGCG 645
 QY 161 AsnIleThrAspTrpMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
 Db 646 AACATCAGACAGACACCATGTGTGTGCCAGCGTGCAGAAAGGGGCAAGAGCTCTCCAG 705
 QY 181 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGly 200
 Db 706 GGTGACTCCGGGGGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 765
 QY 201 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 220
 Db 766 CAGATCGCTGTGGGATGATCAGCCGGAAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 825
 QY 221 AspTrpIleGlnGlnIleThrMetLysAsnAsn 230
 Db 826 GACTGATCCAGGAGAGCATGATGAAGAACAT 855
 RESULT 7
 ID AAF54320 standard; DNA: 1204 BP.
 XX
 AC AAF54320;
 XX
 DT 02-Apr-2001 (first entry)
 XX
 DE DNA encoding protein of the invention #51.
 XX
 KW Secreted; transmembrane; gene therapy; ss.
 XX
 OS Unidentified.
 XX
 PN WO200078961-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 18-FEB-2000; 2000WO-US04342.
 XX
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 16-DEC-1999; 99WO-US30095.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 XX
 PA (GETH) GENENTECH INC.
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;

PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;
PI Watanabe CK, Williams PM, Wood WI;
XX
XX WPI: 2001-071395/08.
XX
XX
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
XX PT useful as hybridization probes, in chromosome and gene mapping and gene
XX therapy -
XX
XX
XX Claim 2; Fig 101; 787pp; English.
XX
XX The present invention relates to secreted and transmembrane proteins.
XX These proteins and the DNA encoding them may be used as hybridization
XX probes, in chromosome and gene mapping and in the generation of
XX anti-sense RNA and DNA. They may also be used to generate either
XX transgenic animals or knockout animals which are in turn useful for
XX development and screening of therapeutically useful reagents.
XX The nucleic acids may also be used in gene therapy.
XX
XX
SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:
Pred. No.: 1,82e-105 Length: 1204
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
22
US-09-856-320A-2_COPY_53_282 (1-230) x AAF54320 (1-1204)

QY 1 ArgIleIleIleSgIyPhegIuCyLysProHISerGInProTrpGInAlaIaleuPhe 20
Db 166 AGGATCATCAAGGGGTTGAGTGCAGACCTCAGCTCCAGCCGTGGAGGAGCCGTGTC 225
QY 21 GlnIySthrIrgIeuleuCySgIyAlaThIleuIleAlaIraIrgItrPleuIleuThIra 40
Db 226 GAAAGAGCGGGCTACTCTGTGGGCGACGCTCATGCCGCCAGATGGCTCTGCACAGCA 285
QY 41 AlAHIScYsLeuLysPProATgTYrIleValHISleuGlyInHISAsnIeugInLysGlu 60
Db 286 GCCCAGCTCTCAAGCCCGCTCATATGTTCACTGGGGAGAGCACAACCTCCAGAGAG 345
QY 61 GluGlyCySgIuInThraIrgThraIaThIrgIuSerPheProHISProGlyIleAsnAsn 80
Db 346 GAGGCGTGTAGCAGACCCGAGCAGCAGCAGTCTCCGCCACCCGCGCTCAACAAAC 405
QY 81 SerIeuProAsnLysAspHISArgAsnAspIleMetIleValIySmetIaIaSerProVal 100
Db 406 AGCCTCCCAACAAGACCAACCCCAATGACATCATGCTGGTGAAGATGGATGCCAGTGC 465
QY 101 SerIleThrTrpAlaValArgProIeuThIleuSerSerArgCySValThraIaGlyThr 120
Db 466 TCCATACACGCGGCTGTGGACCCCTCACCTCTCCACAGCGTGTGCACTGTGGAGCC 525
QY 121 SerCySleuIleSerGlyTrpGlySerThrSerSerProGInIleuArgIeuProHISThr 140
Db 526 AGCTGCTCATTTCCGCTGGGCGACACAGTCACAGCCCGCAGTTACGCTGCTCAACAC 585
QY 141 IeuArgCySAlaIAsnIleThrIleIleGluHISGlnIySgIuSAsnAlaIyrrProGly 160
Db 586 TTGCGATGGCCCAACATCAACATCATTTGAGCACAAGTGTAGAAGCCCTTACCCCGGC 645
QY 161 AsnIleThrAspThrMetValCySAlaSerValGInIuGlyIySAspSerCySgIn 180
Db 646 AACATACAGACACCAATGGTGTGTGCCAGCGTCCAGAGAGGGGCAAGAGCTCTGCCAG 705
QY 181 GlnAspSerGlyIyProIeuValCySAsnGInSerIeuGInIyIleIleSerTrpGly 200
Db 706 GGTGACCTCGGGGCGCTGTGTTGAACCAAGTCTCTTCAAGCATTTATCTCTGGGCG 765
QY 201 GlnAspProCySAlaIleThraIrgIySProGlyValIyThIySValCySlySlyrVal 220

Db 766 CAGATCCGTTGCGAGTACACCCGAAACCTGTGTCTACACGAAAGTCTCAATATGTG 825
QY 221 AspTrpIleGInIuThrMetLysAsnAsn 230
Db 826 GACTGATCCAGAGAGACGATGAAGACAAAT 855

RESULT 8
ABL95664
ID ABL95664 standard; cDNA; 1204 BP.
XX
XX ABL95664;
AC
XX
XX 19-JUL-2002 (first entry)
DT
XX
XX Human angiogenesis related cDNA PRO1279 SEQ ID NO: 207.
DE
XX
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiac; cytosolic; antiangiogenic; hypotensive; vulnary;
KW antiarteriosclerotic; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200208284-A2.
PN
XX
XX 31-JAN-2002.
PD
XX
XX 09-JUL-2001; 2001WO-US21735.
PF
XX
XX 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23528.
PR 07-SEP-2000; 2000US-230978P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0806889.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 28-JUN-2001; 2001WO-US00000.
XX
XX (GERR) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERR/) GERBER H.
PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PAN/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI: 2002-171999/22.
 DR P-PsDB; ABB95526.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 PS Claim 1; Fig 207; 567pp; English.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a coding sequence of the invention.
 XX
 SO Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
 Alignment Scores:
 Pred. No.: 1,82e-105 Length: 1204
 Score: 1263.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0
 US-09-856-320A-2_COPY_53_282 (1-230) x ABL95664 (1-1204)
 QY 1 ArgIlellelysglypnehiucylsypProHisSerGlnProTrpPnaAlaIaleuPhe 20
 DB 166 AGGATCAATCAAGGGGTTGAGTGCAGACCTCACCTCCAGCCCTGGCAGCCCTGTTC 225
 QY 21 GlnlysthrArgleuucysglialaThrLeuIleAlaProArgTrpLeuThrAla 40
 DB 226 GAGAAAGCGGGCTACTCTGTGGGGGAGCGCTCATGCCCCAGATGGCTCGAGACGA 265
 QY 41 AlaHisCysleuysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnysGlu 60
 DB 286 GCCACAGCCTCAAGCCCCCTCATAGTTCACCTGGGCGACACAACCTCCAGAAAGAG 345
 QY 61 GlnGlyCysGlnGlnThrArgTrpAlaThrGluSerPheProHisProGlyPheAsn 80
 DB 346 GAGGGCTGTGAGCAGACCCGAGACCCACTGCTCTCCCAACCCCGGCTTCAACAC 405
 QY 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetLalaserProVal 100
 DB 406 AGCCTCCCAACAAAGCCAGCCGATGACATCATGTGTGAAGATGGATGCCAGTC 465
 QY 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
 DB 466 TTCATACACCGGGCTGTGCGACCCCTCACCTCTCTCAAGCTGTGCACTGTGGCACC 525
 QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnIleuArgLeuProHisThr 140
 DB 526 AGCTGCTCTATTTCGGGCTGGGCGAGCAGCTCCAGCCCACTTACGCTGCTCACC 585

QY 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGly 160
 DB 586 TTGGGATGGCCCAACATCACCATCATTTAGAGCAGCAAGAGTGAAGACGCTACCCGGC 645
 QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGln 180
 DB 646 AACATCACAGACACCAATGAGTGTGTGCCACCGTCGAGAAAGGGGCAAGCACTCCGAC 705
 QY 181 GlyAspSerGlyGlyProLeuValCysAsnGlnSerIleuGlnGlyIleIleSerTrpGly 200
 DB 706 GGTGACTCCGGGGGCTCTGT 765
 QY 201 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 220
 DB 766 CAGATCCGATGGTGGATCACCCGAAAGCCTGTGTCTACACGAAGAGTGTGAATATGTG 825
 QY 221 AspTrpIleGlnGlnThrMetLysAsnAsn 230
 DB 826 GACTGGATCCAGAGAGAGATGAAAGCAAT 855
 RESULT 9
 ABL88175
 ID ABL88175 standard; cDNA, 1204 BP.
 AC
 XX ABL88175;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PRO1279 cDNA sequence SEQ ID NO:207.
 XX
 KW Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
 KW vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial stenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping; gene; ss.
 OS Homo sapiens.
 XX
 PN WO200200690-A2.
 PD
 XX
 PD 03-JAN-2002.
 XX
 PF 20-JUN-2001; 2001WO-US19692.
 XX
 XX 23-JUN-2000; 2000US-213637P.
 XX 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32578.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.

PA (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI: 2002-172001/22.
 DR P-PSDB: AAU83684.
 XX
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 XX
 XX Claim 2; Figure 185; 359pp; English.
 XX
 XX The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABR33536-ABR33657 represent human
 CC PRO protein coding sequences of the invention.
 XX
 XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
 S0
 Alignment Scores:
 Pred. No.: 1.82e-105 Length: 1204
 Score: 1263.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0
 US-09-856-320A-2_COPY_53_282 (1-230) x ABR33628 (1-1204)
 QY 1 Argillelelysglypnehlucylslyspromisserglnprotrpglnalalaaleuphe 20
 DB 166 AGGATCATCAAGGGGTGAGTGCAGAGCCCTGAGCCGAGGAGCCCTGCTC 225
 QY 21 Gltuystrhargleuleucyglalathrleullealaprohlygtrpleuleuthala 40
 DB 226 GAGGAAGACGGCGTACTCTGTGGGGCGAGCTCATCGCCAGATGGCTCTGACAGCA 285
 QY 41 AlahtsCysleuysProargTyrillevalhtsleuglylnhtsAsnleuglnlysglu 60
 DB 286 GCCCACTGCTCAAGCCCGCTACATAGTTCACCTGGGGCGAGCACACCTCCAGAGAG 345
 QY 61 Gluglycysgluglnthargthralathrgluserpheprohtsproglypheasnsn 80
 DB 346 GAGGGCTGTGAGCAGACCCGAGACAGCCACTGAGTCTCCGCCACCCGGGTTCAACAC 405
 QY 81 SerleuproAenlyshAsphhtsArgAsnAspilleMetleuVallyshMetAlaserProval 100
 DB 406 AGCCTCCCAACAAAGACACCGCATATGATCATCTGGTGAAGATGGATCGGCACCTC 465
 QY 101 SerlethrTPAlaValaIarProleuthrleuserSerArgCysValthAlaGlythr 120
 DB 466 TCCATACACTGGGTGTGCGACCCCTCCTCTCTACCGCTGTGTACTGCTGGCAC 525
 QY 121 SerCysleulleSerGlyTyrGlySerThrsSerProglInleuAryleuProhtsThr 140
 DB 526 AGCTGCCATATTCGCGGTGGGAGCAGCAGTCCAGCCCGAGTTAAGCCTCCACACAC 585
 QY 141 LeuArGysAlaAenlleThrllelelhtsGlnlyscysgluAsnAlatyrProgly 160

DB 586 TTGGCATCGCCCAACATACCATCTTGTAGCAGCAGAGGTGTGAGAAAGCCTACCCGCGC 645
 QY 161 AsnlethrAspThrMetValCysAlaSerValGlnGlnGlyLyAspSerCysGln 180
 DB 646 AACATCAGACAGACCATGTGTGTGCCAGCTGCAGAGAGGGGCGAGGATCTCTGCCAG 705
 QY 181 GlyAspSerGlyGlyProleuValCysAsnGlnSerleuglnGlylleIleSerTrpGly 200
 DB 706 GTGCACTCGGGGGGCGCTGTGTGTGAACAGTCTCTTCAAGGCATTAATCTCGGGCGC 765
 QY 201 GlnAspProCysAlaIleThrArglyserProglValIlyThrlyshValCyslyshYrAl 220
 DB 766 CAGATCCGCTGTGCATCACCCGAAAGCTGTGTCTACAGAGAAAGTCTGCAAAATATGTG 825
 QY 221 AspTrpIleGlnGlnThrMetlyshAsn 230
 DB 826 GACTGCATCCAGAGACCATGAAAGCAAT 855
 RESULT 11
 ID ABA83372 standard; cDNA; 1292 BP.
 XX
 AC ABA83372;
 XX
 DT 07-FEB-2002 (first entry)
 DE
 XX Human secreted protein gene 179 SEQ ID NO:189.
 KW Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
 KW dermatological; immunosuppressive; antiinflammato; immunostimulant;
 KW cytosolic; cardiac; vascular; anti-angiogenic; ophthalmological;
 KW neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnery;
 KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
 KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
 KW human immunodeficiency virus; hyperproliferative disorder; wound healing;
 KW Gaucher's disease; cardiovascular disease; Schmitz syndrome; chemotaxis;
 KW Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;
 KW corneal graft neovascularisation; diabetic retinopathy; regeneration;
 KW neurological disorder; Huntington's chorea; Alzheimer's disease;
 KW Parkinson's disease; infectious disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200162891-A2.
 PD 30-AUG-2001.
 XX
 PF 21-FEB-2001; 2001WO-US05614.
 XX
 PR 24-FEB-2000; 2000US-184836P.
 PR 29-MAR-2000; 2000US-193170P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI NI J, Ebner R, Lafleur DM, Moore PA, Olsen HS, Rosen CA;
 PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
 PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AM, Fan P;
 PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;
 PI Zeng Z, Greene JM;
 XX
 DR WPI: 2001-625724/72.
 DR P-PSDB: ABB50479.
 XX
 PT Nucleic acids encoding 207 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -
 XX
 XX Claim 1; Page 1032; 1533pp; English.
 PS
 PS ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
 CC activities based on the tissues and cells the genes are expressed in.

CC Example of these activities include: immunomodulatory; antisclerotic;
 CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 CC anti-HIV; cytostatic; cardiant; anti-angiogenic; ophthalmological;
 CC neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular;
 CC antiparkinsonian; antimicrobial; and vulnerary. (I) and (II) can be used
 CC in gene therapy and vaccine production. (I) and (II) can be used in the
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
 CC Gaucher's disease), cardiovascular diseases (e.g. Sclimtar syndrome,
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA8185 to
 CC ABA8193 and ABB50300 represent sequences used in the exemplification of
 CC the present invention.

XX
 XX Sequence 1292 BP; 319 A; 387 C; 329 G; 253 T; 4 other;
 SQ

Alignment Scores:
 Pred. No.: 2e-105 Length: 1292
 Score: 1263.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x ABA83372 (1-1292)

QY 1 ArgIleIleIysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaIleAlaLeuPhe 20
 Db 267 AGGATCTATCAAGGGGTTGAGTGCAGACCTCCTCCTCCAGCCCTGGCAGGAGCCCTGTTTC 326
 QY 21 GluIysThrIrgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpIleLeuThrAla 40
 Db 327 GAGAGAGCGGGCTACTCTGTGGGGCAGCCTCATCCGCCAGATGCTCTCAGACGCA 386
 QY 41 AlaHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
 Db 387 GCCCAGCTGCTCAAGCCCCCTCATATGTTCCACTGGGGCAGACCAACCTCCAGAGAGAG 446
 QY 61 GluGlyCysGlnGlnIrrArgThrAlaThrGluSerPheProHisProGlyIleAsnAsn 80
 Db 447 GAGGGCTGTAGAGACCCGAGACGCTGAGCTCTCCCAACCCGGCTTCAACAC 506
 QY 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
 Db 507 AGCCTCCCAACAAGACCAACCCCAATGACATCATCTGTGAAGAGCGCATGCCAGTC 566
 QY 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
 Db 567 TCCATCTACCTGGGCTGTGAGACCCCTCACCTCTCCCTCAGCTGTGTGCTGCTGGCACC 626
 QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
 Db 627 AGGTGCTCTATTCCTGGCTGGGAGACGCTCCAGCCCAAGTTACGCCCTGCACACC 686
 QY 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaIleTrpGly 160
 Db 687 TTTCGATGCCCAACATCATCATTTGAGCACCAGAGGTGTAGAAAGCCCTTACCCGGC 746
 QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGln 180
 Db 747 AACATCACAGACACCAATGGGTGTGTCAGAGGTCCAGAGAGGGGCAAGGACCTCTCCGAC 806
 QY 181 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnIleIleSerTrpGly 200
 Db 807 GGTGACTCCGGGGGCTCTGTGTATCAACCAATCTCTTCAAGGCAATTATCTCTGGGCG 866
 QY 201 GlnAspProCysAlaIleThrArgLysProGlyValIleTrpThrLysValCysLysTrpVal 220
 Db 867 CAGGATCCGCTGCTGATCACCAGAAAGCCCTGTGTCTACACGAAAGTCTGCAAAATATGTG 926

QY 221 AspTrpIleGlnGluThrMetLysAsnAsn 230
 Db 927 GACTGATCCAGAGACGATGAGAACAAAT 956

RESULT 12
 ID AAA61763 standard; cDNA; 1301 BP.
 XX
 XX AAA61763:
 XX
 XX 23-OCT-2000 (first entry)
 XX
 XX cDNA encoding human serine protease BSSP6 (hbssP6) SEQ ID NO.1.
 XX
 XX BSSP6; serine protease; human; hbssP6; mouse; mBSSP6; brain;
 KW diagnostic marker; antibody; transgenic animal; Alzheimer's disease;
 KW epilepsy; cancer; inflammation; infertility; pancreatitis;
 KW prostatic hypertrophy; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO200031257-A1.
 XX
 XX 02-JUN-2000.
 XX
 XX 19-NOV-1999; 99WO-JP06476.
 XX
 XX 20-NOV-1998; 98JP-0347802.
 XX
 XX (FUSO) FUSO PHARM IND LTD.
 XX
 XX Nemura H, Okui A, Kominami K, Yamaguchi N, Mitsui S;
 DR P-PSDB; AAB11712.
 XX
 XX MPI: 2000-40067/34.
 XX
 XX P-PSDB; AAB11712.
 XX
 XX Serine protease BSSP6, useful in detecting homologs, mutants and
 PT polymorphic variants as markers for diagnosis of Alzheimer's disease,
 PT epilepsy, cancer, inflammation, infertility and prostate hypertrophy,
 PT using blood or other tissues
 XX
 XX Claim 2; Page 67-69; 94pp; Japanese.

XX
 XX The invention relates to novel serine proteases designated BSSP6
 CC (AAB11712-B11714), and to nucleic acids encoding them (AAA61763-A61765).
 CC The invention also relates to vectors and transformants comprising BSSP6
 CC nucleic acids; transgenic animals in which the expression level of BSSP6
 CC can be varied; and an mBSSP6 knockout mouse. The invention additionally
 CC encompasses anti-BSSP6 antibodies and methods of production of such
 CC antibodies, methods of BSSP6 detection using the antibodies, and the
 CC use of BSSP6 proteins or fragments as diagnostic markers for certain
 CC medical conditions. Nucleotides encoding BSSP6 were initially
 CC isolated in a human brain cDNA library using degenerate PCR primers
 CC (AAA61795-A61796) based on conserved regions of serine proteases. The
 CC BSSP6 serine proteases and nucleotides encoding them are useful in
 CC detecting homologues, mutants and polymorphic variants in biological
 CC samples (e.g., blood, urine, brain, prostate gland, placenta, testis
 CC and spleen) as diagnostic markers for conditions such as Alzheimer's
 CC disease, epilepsy, cancer, inflammation, infertility and prostatic
 CC hypertrophy. Sequences AAA61763 and AAA61765 represent cDNAs encoding
 CC human BSSP6 variants (hbssP6), and sequence AAA61764 represents cDNA
 CC encoding murine BSSP6 (mBSSP6).
 XX

SQ Sequence 1301 BP; 332 A; 387 C; 330 G; 252 T; 0 other;

Alignment Scores:
 Pred. No.: 2.01e-105 Length: 1301
 Score: 1263.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x AAA61763 (1-1301)

QY 1 Argillelelysglypneglucyslysprohisserglnprotrpglnalaaleuphe 20
 DB 269 AGGATCATCAAGGGGTTGAGTGCAGAGCTCAGCCCTGCGAGGAGCCCTGTC 328

QY 21 GlulysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 40
 DB 329 GAGAAAGAGCGCGTACTGCTGGGGCGAGCTCATCCGCCAGATGCTCCTGCACAGA 388

QY 41 AlaHisCysLeuysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnysglu 60
 DB 389 GCCCACTGCTCAAGCCCCGCTACATAGTTCACTGGGGGAGACAACTCCAGAAAGAG 448

QY 61 GlulGlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsn 80
 DB 449 GAGGGCTGTGAGCAGACCCGGAGACCCAGTCTCTCCGCCAGCCGCTTCAACAG 508

QY 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
 DB 509 AGCTTCCCAACAAAGACACCCAGCATGATGCTGTGAAGATGGCATCGGCACTC 568

QY 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
 DB 569 TCCATCACTGGCTGTGCGAGCCCTCACCTCTCCTCACGCTGTGCTGCGAGCC 628

QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
 DB 629 AGCTGCCCATTTCCGGCTGGGGGAGCAGCTCCAGCCCGATAGCTCTCCTCACACC 688

QY 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTrpProGly 160
 DB 689 TTGGGATGCGCCCAATCATCATGAGCAGCAGAAAGTGTGAAGCGCTACCCGCGC 748

QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
 DB 749 AACATCACAGACCATGCTGTGCGAGCTGAGGAGGAGGAGGAGGAGCTCTGCGAG 808

QY 181 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 200
 DB 809 GGTGATCTCGGGGGCCCTGCTGTGTAACAGTCTCTCAAGCATTAATCTCTGGGGC 868

QY 201 GlnAspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTrpVal 220
 DB 869 CAGATCCGTCGTCGATCAGCAGCCGGAAGCTGTGTCTACGAGAAAGCTGCAAAATATGTG 928

QY 221 AspTrpIleGlnGluThrMetLysAsn 230
 DB 929 GACTGATCCAGAGAGCATGAGAACAAT 958

RESULT 13
 AA30222
 ID AA30222 standard; cDNA; 1314 BP.
 AC AA30222;
 XX 11-FEB-2000 (first entry)
 DE cDNA encoding a human prostate-associated serum protease (PRASP).
 KW Human; prostate-associated serum protease; PRASP; neuropsin; PSA;
 KW Incyte clone 2723646; reproductive disorder; cancer;
 KW abnormal prolactin production; infertility; tubal disease;
 KW ovulatory defect; endometriosis; polycystic ovary syndrome;
 KW autoimmune disorder; ectopic pregnancy; breast cancer;
 KW abnormal spermatogenesis; testicular cancer; adenocarcinoma; leukaemia;
 KW lymphoma; melanoma; myeloma; sarcoma; teratocarcinoma; ss.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 CDS 128..976

FT FT /*tag- a
 FT FT /product= "prostate-associated serum protease"
 FT FT 146..181
 FT FT /*tag- b
 FT FT /note= "these nucleotides are separately claimed
 FT FT misc.feature 344..382
 FT FT /*tag- c
 FT FT /note= "these nucleotides are separately claimed
 FT FT misc.feature 551..589
 FT FT /*tag- d
 FT FT /note= "these nucleotides are separately claimed
 FT FT under claim 10"
 PN WO9941387-A2.
 XX
 XX 19-AUG-1999.*
 PD
 XX
 XX 05-FEB-1999; 99WO-US02571.
 PF
 XX
 PR 17-FEB-1998; 98US-0025059.
 XX
 XX (INCY-) INCYTE PHARM INC.
 PA
 PI Tang YT, Corley NC, Guegler KJ;
 XX
 DR WPI: 2000-012993/01.
 DR P-PSDB: AAY43636.
 XX
 PT New prostate-associated serum protease and polynucleotides which
 PT identify and encode PRASP, useful for treating reproductive disorders
 PT and cancer
 XX
 PS Claim 7; Fig 1A-D; 67pp; English.
 XX
 CC The present sequence encodes a human prostate-associated serum protease
 CC (PRASP). The protein shows homology to neuropsin, a brain-specific
 CC protease in mice, and PSA, a prostate-specific protease in humans.
 CC Nucleic acids encoding PRASP were first identified in Incyte clone
 CC 2723646 from the lung tumour cDNA library. Pharmaceutical compositions
 CC containing PRASP, or antibodies to PRASP, and mimetics, agonists,
 CC antagonists or inhibitors of PRASP, are used for treating or preventing
 CC a reproductive disorder or cancer. Examples of reproductive disorder
 CC include, abnormal prolactin production, infertility, tubal disease,
 CC ovulatory defects, endometriosis, polycystic ovary syndrome, autoimmune
 CC disorders, ectopic pregnancy, breast cancer, abnormal spermatogenesis
 CC and testicular cancer. Examples of cancers which may be treated or
 CC prevented include adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma,
 CC sarcoma, teratocarcinoma, and cancers of the adrenal gland, bladder,
 CC bone, bone marrow, brain, breast, cervix, penis, prostate, salivary
 CC glands, skin, spleen, testis, thymus, thyroid and uterus. A vector
 CC capable of expressing PRASP or an agonist which modulates the activity of
 CC PRASP may be administered to treat or prevent a reproductive disorder or
 CC cancer.
 XX
 SQ Sequence 1314 BP; 320 A; 400 C; 337 G; 257 T; 0 other;
 XX

Alignment Scores:
 Pred. No.: 2.04e-105 Length: 1314
 Score: 1263.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x AA30222 (1-1314)

QY 1 Argillelelysglypneglucyslysprohisserglnprotrpglnalaaleuphe 20
 DB 284 AGGATCATCAAGGGGTTGAGTGCAGAGCTCAGCCCTGCGAGGAGCCCTGTC 343

QY 21 GlulysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 40

|||||
Db 344 GAGAGACGGCGCTACTGTGGGGGACGCTATCGCCCCCAAGATGCTCTGCACAGCA 403
QY 41 AlahiscysleuylsProArgTyrIleValHisleuGIylnHisAsnleuGIlnLysGIu 60
Db 404 GCCACAGCGCTCAAGCCCCCTACATAGTTCACCTGGGGACGACCAACCTCCAGAAAGAG 463
QY 61 GluGIyCysGIuGIlnHrArgHrAlaThrGluSerPheProHisProGIyPheAsnAsn 80
Db 464 GAGGCGGTGAGACAGACCCGACAGCCAGTACGTCTTCCCCCAGCCCCGCTTCAACAC 523
QY 81 SerleuProAsnLysAspHisArgAsnAspIleMetleuValLysMetIleAsnProVal 100
Db 524 AGCTCCCAACAAAGACACCGACATGACATCATGCTGTGAAGATGGCATGCCAGTC 583
QY 101 SerIleHrTrpAlaValAlaProleuThrLeuSerSerArgCysValThrAlaGIyThr 120
Db 584 TTCATACCGCGGGCTGTGGACACCCCTACCTCTCCACAGCTGTGCATCGCTGGAC 643
QY 121 SerCysleuIleSerGIyTrpGIySerThrSerSerProGIlnleuArgleuProHisThr 140
Db 644 AGCTGCTCATTTCCGCGTGGGACAGACCTCCAGCCCCAGTTACGCTGCTGCACACC 703
QY 141 LeuArgCysAlaAsnIleThrIleleGIlnHisGIlnLysCysGIuAsnAlaTyrProGIy 160
Db 704 TTCGATGCGCCCAACATCACATCATTTAGACACAGAAAGTGAAGACGCTACCCGCG 763
QY 161 AsnIleHrAspThrMetValCysAlaSerValGIlnGIuGIyLysAspSerCysGIln 180
Db 764 AACATCACACACACATCATGTGTGTCCAGCGTGCAGAAAGGGGACCAAGACTCTGCGAC 823
QY 181 GlyAspSerGIyLysProleuValCysAsnGIlnSerleuGIlnGIyIleIleSerTrpGIy 200
Db 824 GTTGACTCCCGGGGCGCTGTGTGTGAACCACTCTTCAAGGACATTAATCTCTGGGCG 883
QY 201 GluAspProCysAlaIleThrArgLysProGIyValTyrThrLysValCysLysTyrVal 220
Db 884 CAGGATTCGGTGTGCATCACCCGAAAGCTGTGTCTACGAAAGTGTGCAATATATGTG 943
QY 221 AspTrpIleGIlnGIuThrMetLysAsnAsn 230
Db 944 GACTGATCCAGAGACGATGAAGAACAT 973
RESULT 14
AAV84589 standard; DNA; 1146 BP.
ID AAV84589;
AC XX
XX AAV84589;
DT 01-MAR-1999 (first entry)
XX
XX Human secreted protein gene 179 clone HETBX14.
XX
XX Human: secreted protein; fusion protein; gene therapy; protein therapy;
KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KM developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KM immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KM inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;
KM cognitive disorder; schizophrenia; prostate; obesity; osteoclasts; thymus;
KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
XX
PN WO9854963-A2.
XX
PD 10-DEC-1998.
XX
XX 04-JUN-1998; 98WO-US11422.
PF
XX 18-DEC-1997; 97US-0070923.
PR 06-JUN-1997; 97US-0048877.
PR 06-JUN-1997; 97US-0048881.

PR 06-JUN-1997; 97US-0048884.
PR 06-JUN-1997; 97US-0048893.
PR 06-JUN-1997; 97US-0048896.
PR 06-JUN-1997; 97US-0048899.
PR 06-JUN-1997; 97US-0048915.
PR 06-JUN-1997; 97US-0048949.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048972.
PR 06-JUN-1997; 97US-0049020.
PR 06-JUN-1997; 97US-0049375.
PR 05-SEP-1997; 97US-0057628.
PR 05-SEP-1997; 97US-0057635.
PR 05-SEP-1997; 97US-0057644.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057657.
PR 05-SEP-1997; 97US-0057661.
PR 05-SEP-1997; 97US-0057667.
PR 05-SEP-1997; 97US-0057761.
PR 05-SEP-1997; 97US-0057764.
PR 05-SEP-1997; 97US-0057770.
PR 05-SEP-1997; 97US-0057775.
PR 05-SEP-1997; 97US-0057778.
PR 06-JUN-1997; 97US-0048875.
PR 06-JUN-1997; 97US-0048878.
PR 06-JUN-1997; 97US-0048882.
PR 06-JUN-1997; 97US-0048885.
PR 06-JUN-1997; 97US-0048894.
PR 06-JUN-1997; 97US-0048897.
PR 06-JUN-1997; 97US-0048900.
PR 06-JUN-1997; 97US-0048916.
PR 06-JUN-1997; 97US-0048962.
PR 06-JUN-1997; 97US-0048970.
PR 06-JUN-1997; 97US-0048974.
PR 06-JUN-1997; 97US-0049373.
PR 05-SEP-1997; 97US-0057584.
PR 05-SEP-1997; 97US-0057625.
PR 05-SEP-1997; 97US-0057642.
PR 05-SEP-1997; 97US-0057645.
PR 05-SEP-1997; 97US-0057648.
PR 05-SEP-1997; 97US-0057651.
PR 05-SEP-1997; 97US-0057662.
PR 05-SEP-1997; 97US-0057668.
PR 05-SEP-1997; 97US-0057762.
PR 05-SEP-1997; 97US-0057765.
PR 05-SEP-1997; 97US-0057771.
PR 05-SEP-1997; 97US-0057776.
PR 06-JUN-1997; 97US-0048876.
PR 06-JUN-1997; 97US-0048880.
PR 06-JUN-1997; 97US-0048883.
PR 06-JUN-1997; 97US-0048892.
PR 06-JUN-1997; 97US-0048895.
PR 06-JUN-1997; 97US-0048898.
PR 06-JUN-1997; 97US-0048901.
PR 06-JUN-1997; 97US-0048917.
PR 06-JUN-1997; 97US-0048963.
PR 06-JUN-1997; 97US-0048971.
PR 06-JUN-1997; 97US-0049019.
PR 06-JUN-1997; 97US-0049374.
PR 05-SEP-1997; 97US-0057627.
PR 05-SEP-1997; 97US-0057634.
PR 05-SEP-1997; 97US-0057643.
PR 05-SEP-1997; 97US-0057646.
PR 05-SEP-1997; 97US-0057649.
PR 05-SEP-1997; 97US-0057654.
PR 05-SEP-1997; 97US-0057666.
PR 05-SEP-1997; 97US-0057760.
PR 05-SEP-1997; 97US-0057763.
PR 05-SEP-1997; 97US-0057769.
PR 05-SEP-1997; 97US-0057774.
PR 05-SEP-1997; 97US-0057777.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX

PI Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA;
PI Fan P, Feng P, Ferrie AM, Fischer CL, Florence C;
PI Florence K, Greene JM, Hu J, Kyaw H, Lafleur DM;
PI Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM;
PI Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
XX
DR WPI: 1999-059865/05.
DR P-PSDB: AAM88712, AAM89041, AAM89042, AAM89043.
XX
XX New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 4: Page 441-442; 772pp: English.
XX
XX The invention relates to nucleic acid sequences (AAV84411 to AAV84633)
CC encoding human secreted proteins (AAM88534 to AAM88765). The secreted
CC protein gene sequences are deposited with the ATCC under deposit numbers
CC ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
CC 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host
CC cells comprising recombinant vectors containing the nucleic acid
CC sequences are used for the recombinant production of the secreted
CC proteins. The polynucleotide and amino acid sequences are useful for are
CC useful for preventing, treating or ameliorating medical conditions e.g.
CC by protein or gene therapy. Pathological conditions can be also
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the polynucleotides, based on
CC which tissues they are most highly expressed in, and include developing
CC products for the diagnosis or treatment of cancer, neurodegenerative
CC disorders, developmental abnormalities and foetal deficiencies, blood
CC disorders, tumours, leukemias, diseases of the immune system, autoimmune
CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
CC restenosis, prostate diseases, obesity, disorders involving osteoclasts
CC such as osteoporosis, arthritis or malignancies, diseases of testes,
CC lung or thymus, digestive/endocrine disorders, infections and AIDS. The
CC polypeptides are also useful for identifying their binding partners.
CC The present sequence represents a gene encoding a human secreted protein
CC (see descriptor line for gene number and clone identification).
XX
XX Sequence 1146 BP; 282 A; 347 C; 272 G; 237 T; 8 other;
S0

Alignment Scores:
Pred. No.: 1.39e-104 Length: 1146
Score: 1253.00 Matches: 228
Percent Similarity: 99.13% Conservative: 2
Best Local Similarity: 99.13% Mismatches: 2
Query Match: 99.21% Indels: 0
DB: 20 Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x AAV84589 (1-1146)

QY 1 Argillelelysglypneclucylslyprohisserginprotrpglnalalaaleuphe 20
DB 121 AGGATCATCAAGGGGTTGAGTGCAGAGCTCCAGCCCTGGCAGGACCCCTGTTC 180

QY 21 GlutylthraaleuleucysglYAlaThrleulealaProAqTyrPleuleThra 40
DB 181 GAGAAAGCGCGCTACTCTGTGGGGCAGCGTCAATCGCCCAATGCTCTTACAGCA 240

QY 41 AlahtscysleuysProAqTyrTleValhlsleuglgnhlsasnleuglnlysglu 60
DB 241 GCCCAGTCCCTCAAGCCCGCTACATAGTTCACCTGGGGGAGCAACCTCCAGAGAG 300

QY 61 GlunglyssgluglnthraArgThralaThrcluSerPheprohlsproglYpheasn 80
DB 301 GAGGAGCTGTGACAGCCCGGAGCCACTGATGTCCTTCCCAACCCCGGCTTCAACAC 360

QY 81 SerleuproAenLysAspRhlAArgAsnApRlleMetleuValysMetAlaSerProval 100
DB 361 AGCTTCCCAACAAAGACACACCGCATCATCATGCTGTGTAAGATNGCATGCCAGTC 420

QY 101 SerllerhTrpAlaValArgProleuThrLeuSerSerArgCysValThraAlaGlyThr 120
DB 421 TCCATCACCTGGGCTGTGCGACCCCTCCTCTCCAGCTGTGTCACGTGGCACCC 480

QY 121 SerCysleuileleserGlyTnrglyserThrSerSerProGlnleuArgleuProhlsThr 140
DB 481 AGCTGCTCATATTTCCGGCTGGGGCAGMACGTCCACCCCGAGTAAAGCCTGCCATCACCC 540

QY 141 LeuArgCysAlaAsnIleThrIleleGlnhlsGlnlyscysGluAsnAlaTyrProgly 160
DB 541 TTGSATCCGCCACATCATCATCATTTAGACACCGAAGTGTGAGAACGCTACCCCGCC 600

QY 161 AsnllerhAspRhlMetValCysAlaSerValGlnGlyGlyLysAspSerCysGln 180
DB 601 AACATCACAGACACCATGTGTGTGCCAGCTGCAGAAAGGGGCGAACGACTCTGCCAG 660

QY 181 GlyAspSerGlyGlyProleuValCysAsnGlnSerleuGlnGlyIleIleSerTrpGly 200
DB 661 GGTGACTCCGGGGGCGCCCTGCTGTGAACAGTCTTTCAAAGGCAATTATTCCTGGGGCC 720

QY 201 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 220
DB 721 CAGATCCGTTGCGATACACCGAAGCCTGTGTCTACAGMAAGTGTGCAATATGTG 780

QY 221 AspTrpIleGlnGluThrMetLysAsnAsn 230
DB 781 GACTGGATCCAGAGACGATGAGAACAT 810

RESULT 15
ABA83430
ID ABA83430 standard; cDNA; 1146 BP.
XX
XX ABA83430;
AC
XX 07-FEB-2002 (first entry)
XX
XX Human secreted protein gene 179 SEQ ID NO:247.
DE
XX
XX Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
KW dermatological; immunosuppressive; antiinflammatory; immunostimulant;
KW cyrostatic; cardiant; vascular; anti-angiogenic; ophthalmological;
KW neuroprotective; noctropic; anticonvulsant; antialzheimers; vulnertary;
KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
KW human immunodeficiency virus; hyperproliferative disorder; wound healing;
KW Chagar's cardiomyopathy; coronary arteriosclerosis; angiotensin disorder;
KW corneal graft neovascularisation; diabetic retinopathy; regeneration;
KW neurological disorder; Huntington's chorea; Alzheimer's disease;
KW Parkinson's disease; infectious disease; s9.
XX
XX Homo sapiens.
OS
XX
XX W0200162891-A2.
PN
XX
XX 30-AUG-2001.
PD
XX
XX 21-FEB-2001; 2001WO-US05614.
PE
XX
XX 24-FEB-2000; 2000US-184836P.
PR
XX
XX 29-MAR-2000; 2000US-193170P.
PA
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ni J, Ebner R, Lafleur DM, Moore PA, Olsen HS, Rosen CA;
PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AM, Fan P;
PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;
PI Zeng Z, Greene JM;
XX
XX WPI: 2001-625724/72.
DR
XX P-PSDB: ABB50537.

PT Nucleic acids encoding 207 human secreted polypeptides, useful for
PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's
PT disease and diabetic retinopathy -
XX
PS Claim 1; Page 1072-1073; 1533pp; English.

[illegible]

Alignment Scores:	
Pred. No.:	1.39e-104
Score:	1253.00
Percent Similarity:	99.13%
Best Local Similarity:	99.13%
Query Match:	99.21%
DB:	22
	Gaps: 0
	Length: 1146
	Matches: 228
	Conservative: 0
	Mismatches: 2
	Indels: 0

US-09-856-320A-2_COPY_53_282 (1-230) x ABA83430 (1-1146)

QY 1 ArgIleIleIysGSLyPheGLICysLysProHissSerGlnProTrpGlnAlaIlePhe 20

Db 121 AGGATCATCAAGGGGGTTTCAGTGCAGAACCTTCACTCCAGCCCTGGCAGGACCCCTGTTTC 180

QY 21 GILuYSThrArgLeuLeuCysGLyAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 40

Db 181 GAGAAAGACGGCGTACTCTGTGGGGGACGGCTCATCCGCCAGATGGCTGTGACAGA 240

QY 41 AlaHisCysLeuLysProArgTrpIleValHisLeuGLyIleHisAsnLeuGlnLysGlu 60

Db 241 GCCCAGCTGCCTCAAGCCCCGGCTACATGTTTACCTGGGGCAGGACAAACCTCCAGAAAGGAC 300

QY 61 GILuGLyCysGluGlnThrArgTrpAlaThrGlnSerPheProHisProGlyPheAsn 80

Db 301 GAGGCTGTGTAGCAGACCCGGACAGCCAGCTGAGTCTTCCCCACCCGGCTTCACACAC 360

QY 81 SerLeuProAsnLysAspHisArgAsnAspIleLeuLeuValLysMetAlaSerProVal 100

Db 361 AGCCTCCCAACAAAGACCCACCGCAATGACATGCTGGTGAAGATGCATGCCAGTCC 420

QY 101 SerIleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgGlyValThrAlaGlyThr 120

Db 421 TTCATCACTGGGGCTGTGGCAGACCCCTCACTCCCTCCAGCGTGTGCATCGTGGCAC 480

QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140

Db 481 AGCTGTCTCATTTCCGGCTGGGGGACGAGAACCTCCAGCCCCAGTTAGCGCTTCACACCC 540

QY 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGly 160

Db 541 TTGGATTCGGCGCAACATCCACATCATTTGACACACAGAAAGTGTAGAAAGCCTACCGGGC 600

QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGln 180

Db	601	AACATCACAGACACCACATGAGTGTCGCCAGCGTGACGAGAGAGGGGCAAGACACTCTGGCAC	660
Qy	181	GIYAspSerGIYglYProLeuValCysAsnGInSerLeuGInglYIleIleSerTPGly	200
Db	661	GGTAGACTCCGGGGGGGCCCTCTGGTGTCTGTAAACCAAGCTCTCTCAAGGACATTAATCTCTGGGGC	720
Qy	201	GIInAspProCysAlaIleThrArgLysProGlyAlaIYrThrLysValCysLysTYrVal	220
Db	721	CAGATCCGCTGTGGGATCCACCCGAAACCTGGGTCTACACGAAGTCTGCCAAATATGTG	780
Qy	221	AspTrpIleGInGluThrMetLysAsnAsn	230
Db	781	GACTGATCCAGAGACGATGAAAGACAAT	810

Search completed: December 23, 2002, 14:32:45
Job time : 307 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2002, 14:17:42 ; Search time 36 Seconds

(without alignments)
187,980 Million cell updates/sec

Title: US-09-856-320A-2_COPY_53_282

Perfect score: 1263
Sequence: 1 RIITGFECKVHSPQWMAALF.....GVYTKCKYVDIQTWKNN 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1263	100.0	282	3	US-09-025-059-1
2	1232	97.5	282	4	US-08-944-483-24
3	1221.5	96.7	289	4	US-09-386-642-14
4	686	54.3	260	3	US-09-025-059-3
5	683	54.1	260	3	US-09-070-526-2
6	675	53.4	260	4	US-09-008-271A-7
7	673.5	53.3	288	4	US-09-386-642-13
8	597.5	47.3	268	2	US-08-824-874-1
9	587.5	47.3	268	4	US-09-210-084-1
10	536.5	47.2	263	2	US-08-790-137-4
11	536.5	47.2	263	2	US-08-824-874-5
12	536.5	47.2	263	3	US-08-807-151-5
13	536.5	47.2	263	4	US-09-210-084-5
14	536.5	47.2	263	4	US-09-478-957-5
15	589	46.6	246	2	US-08-978-404B-44
16	582.5	46.1	244	3	US-08-768-859A-10
17	582.5	46.1	244	3	US-08-767-820A-10
18	582.5	46.1	244	3	US-08-622-046B-16
19	582.5	46.1	244	4	US-09-100-264-5
20	582.5	46.1	261	3	US-08-768-859A-6
21	582.5	46.1	261	3	US-08-767-820A-6
22	582.5	46.1	261	3	US-08-622-046B-14
23	582.5	46.1	261	4	US-09-100-264-7
24	582.5	46.1	261	4	US-08-983-075D-7
25	579.5	45.9	244	3	US-08-622-046B-5
26	579.5	45.9	261	3	US-08-768-859A-19
27	579.5	45.9	261	3	US-08-767-820A-19

28	579.5	45.9	261	3	US-08-622-046B-3	Sequence 3, Appl1
29	579	45.8	244	1	US-08-361-395-1	Sequence 1, Appl1
30	579	45.8	247	2	US-08-956-267A-2	Sequence 2, Appl1
31	578.5	45.8	244	5	PCT-US95-06157-10	Sequence 6, Appl1
32	578.5	45.8	261	5	PCT-US95-06157-6	Sequence 10, Appl1
33	578	45.8	237	2	US-08-978-404B-45	Sequence 45, Appl1
34	577.5	45.7	237	3	US-08-768-859A-16	Sequence 16, Appl1
35	577.5	45.7	237	3	US-08-767-820A-16	Sequence 12, Appl1
36	577.5	45.7	237	3	US-08-622-046B-12	Sequence 37, Appl1
37	577.5	45.7	237	4	US-08-944-483-37	Sequence 1, Appl1
38	577.5	45.7	237	4	US-09-100-264-1	Sequence 8, Appl1
39	577.5	45.7	238	3	US-08-768-859A-8	Sequence 8, Appl1
40	577.5	45.7	238	3	US-08-767-820A-8	Sequence 8, Appl1
41	577	45.7	228	1	US-08-278-091-7	Sequence 7, Appl1
42	577	45.7	228	1	US-08-483-859-7	Sequence 7, Appl1
43	577	45.7	228	1	US-08-472-173-7	Sequence 7, Appl1
44	577	45.7	228	2	US-08-487-167-7	Sequence 7, Appl1
45	577	45.7	228	2	US-08-482-816-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-09-025-059-1
Sequence 1, Application US/09025059
Patent No. 6075136
GENERAL INFORMATION:
APPLICANT: Tang, Y. nom
APPLICANT: Corley, Nell C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,059
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0481 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGTU10
CLONE: 2723646
US-09-025-059-1
Query Match 100.0%; Score 1263; DB 3; Length 282;
Best Local Similarity 100.0%; Pred. No. 2.3e-126;

Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIIFGECRPHSOPWQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHIGOHNLQKE 60
Db 53 RIIFGECRPHSOPWQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHIGOHNLQKE 112
QY 61 EGCQRTATSESPHPGFNSLPKNDHRNDIMLVKASPVSTWAVRPLTLSSRCVTAGT 120
Db 113 EGCQRTATSESPHPGFNSLPKNDHRNDIMLVKASPVSTWAVRPLTLSSRCVTAGT 172
QY 121 SCLISGWSSTSPQLRPLPRLRCANITIIHOKCENAYPGNITDITWVCASVOEGKDSQ 180
Db 173 SCLISGWSSTSPQLRPLPRLRCANITIIHOKCENAYPGNITDITWVCASVOEGKDSQ 232
QY 181 GDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTKVCKYVDWIOETMKN 230
Db 233 GDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTKVCKYVDWIOETMKN 282

RESULT 2
US-08-944-483-24
; Sequence 24, Application US/08944483
; Patent No. 6232456

GENERAL INFORMATION:

APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.

TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS

TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/944,483

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6183.US.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 248 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: NO. 62324566

US-08-944-483-24

Query Match 97.5%; Score 1232; DB 4; Length 248;

Best Local Similarity 99.1%; Pred. No. 3.7e-123;
Matches 228; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 RIIFGECRPHSOPWQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHIGOHNLQKE 60
Db 21 RIIFGECRPHSOPWQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHIGOHNLQKE 78
QY 61 EGCQRTATSESPHPGFNSLPKNDHRNDIMLVKASPVSTWAVRPLTLSSRCVTAGT 120
Db 79 EGCQRTATSESPHPGFNSLPKNDHRNDIMLVKASPVSTWAVRPLTLSSRCVTAGT 138
QY 121 SCLISGWSSTSPQLRPLPRLRCANITIIHOKCENAYPGNITDITWVCASVOEGKDSQ 180
Db 139 SCLISGWSSTSPQLRPLPRLRCANITIIHOKCENAYPGNITDITWVCASVOEGKDSQ 198
QY 181 GDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTKVCKYVDWIOETMKN 230
Db 199 GDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTKVCKYVDWIOETMKN 248

RESULT 3
US-09-386-642-14
; Sequence 14, Application US/09386642
; Patent No. 6420157

GENERAL INFORMATION:

APPLICANT: Darrow, Andrew
APPLICANT: OL, Jensen
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14

LENGTH: 289

TYPE: PRP

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Fusion gene

OTHER INFORMATION: with homo sapien serine protease catalytic domain

US-09-386-642-14

Query Match 96.7%; Score 1221.5; DB 4; Length 289;

Best Local Similarity 96.5%; Pred. No. 6.1e-122;

Matches 223; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 1 RIIFGECRPHSOPWQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHIGOHNLQKE 59
Db 51 RIIFGECRPHSOPWQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHIGOHNLQKE 110
QY 60 EGCQRTATSESPHPGFNSLPKNDHRNDIMLVKASPVSTWAVRPLTLSSRCVTAGT 119
Db 111 EGCQRTATSESPHPGFNSLPKNDHRNDIMLVKASPVSTWAVRPLTLSSRCVTAGT 170
QY 120 TSCLISGWSSTSPQLRPLPRLRCANITIIHOKCENAYPGNITDITWVCASVOEGKDSQ 179
Db 171 TSCLISGWSSTSPQLRPLPRLRCANITIIHOKCENAYPGNITDITWVCASVOEGKDSQ 230
QY 180 QDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTKVCKYVDWIOETMKN 230
Db 231 QDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTKVCKYVDWIOETMKN 281

RESULT 4
US-09-025-059-3
; Sequence 3, Application US/09025059
; Patent No. 6075136

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Corley, Neil C.

APPLICANT: Guegler, Karl J.

TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE


```

;
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheila
; REGISTRATION NUMBER: 41,201
;
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELEPHONE: 650-845-4166
; TELEFAX: 650-855-0555
;
; INFORMATION FOR SEQ ID NO: 7:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; IMMEDIATE SOURCE:
; LIBRARY: COLN0T27
; CLONE: 1798496
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
US-09-008-271A-7

Query Match 53.4%; Score 675; DB 4; Length 260;
Best Local Similarity 51.1%; Pred. No. 6,8e-64;
Matches 115; Conservative 43; Mismatches 65; Indels 2; Gaps 2;

QY 1 RIITGFECKPHSOPWQALFEKTRLLCGATLLAPRLTLTAHCLKPRYIVHLCGHNLOKE 60
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 32 KYVGNHCQPHSQPMQALFQCGQLCGVLVGNNVLTAAHCKKPKYIVRLGDHSLON 91
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 61 EGCEQRTATSPHPHGFNNSLPNKDRNDIMLVKASPVSTWAVRPLTLSSRCVTAGT 120
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 92 DGEQDEIPVVGSTIPHCYNSS-DVEDHNDMLQLRDQASIGSKVPISLADHCTQPG 150
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 121 SCLISGSGTSSPOLRLPHRLKCANITIEHOKCEANVPGNITDTWVCASVQSGKNSCQ 180
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 151 KCTVSGNGVTSPRENFPDLNCAEVKIPQKCEADYPGQITDGMVCASSSKGA-DTCQ 209
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 181 GDSGGPLVCNOSLOGIISWGQDPCATRRKPGVYTKVCKYVDWIOE 225
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 210 GDSGGPLVCNOLGIGITWSGSDPCGRSDKRGVYTNICRYLDWIKK 254
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 7
US-09-386-642-13
; Sequence 13, Application US/09386642
; Patent No. 6420157
;
; GENERAL INFORMATION:
; APPLICANT: Dartow, Andrew
; APPLICANT: Q1, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```

;
; FEATURE:
;
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-13

Query Match 53.3%; Score 673.5; DB 4; Length 288;
Best Local Similarity 51.3%; Pred. No. 1.1e-63;
Matches 116; Conservative 43; Mismatches 64; Indels 3; Gaps 3;

QY 1 RIITGFECKPHSOPWQALFEKTRLLCGATLLAPRLTLTAHCLKPRYIVHLCGHNLOK 59
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 51 KYVGNHCQPHSQPMQALFQCGQLCGVLVGNNVLTAAHCKKPKYIVRLGDHSLON 110
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 60 EGCEQRTATSPHPHGFNNSLPNKDRNDIMLVKASPVSTWAVRPLTLSSRCVTAG 119
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 111 KDPEQDEIPVVGSTIPHCYNSS-DVEDHNDMLQLRDQASIGSKVPISLADHCTQPG 169
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 120 TSCGISGSGTSSPOLRLPHRLKCANITIEHOKCEANVPGNITDTWVCASVQSGKNSC 179
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 170 QKCTVSGNGVTSPRENFPDLNCAEVKIPQKCEADYPGQITDGMVCASSSKGA-DTC 228
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 180 GDSGGPLVCNOSLOGIISWGQDPCATRRKPGVYTKVCKYVDWIOE 225
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 229 GDSGGPLVCNOLGIGITWSGSDPCGRSDKRGVYTNICRYLDWIKK 274
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 8
US-08-824-874-1
; Sequence 1, Application US/08824874
; Patent No. 5962300
;
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KERANOT02
; CLONE: 820694
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; US-08-824-874-1

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Best Local Similarity -49.18; Pred. No. 1.2e-55;
Matches 110; Conservative 39; Mismatches 68; Indels 7; Gaps 4;

[illegible]

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1      RESULT 9
2      US-09-210-084-1
3      Sequence 1, Application US/09210084
4      Patent No. 6197511
5      GENERAL INFORMATION:
6      APPLICANT: Hillman, Jennifer L.
7      APPLICANT: Lal, Preeti
8      TITLE OF INVENTION: NOVEL KALLIKREIN
9      NUMBER OF SEQUENCES: 5
10     CORRESPONDENCE ADDRESS:
11     ADDRESSSEE: Incyte Pharmaceuticals, Inc.
12     STREET: 3174 Porter Drive
13     CITY: Palo Alto
14     STATE: CA
15     COUNTRY: USA
16     ZIP: 94304
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: Diskette
19     COMPUTER: IBM Compatible
20     OPERATING SYSTEM: DOS
21     SOFTWARE: FASTSEQ for Windows Version 2.0
22     CURRENT APPLICATION DATA:
23     APPLICATION NUMBER: US/09/210,084
24     FILING DATE:
25     CLASSIFICATION:
26     PRIOR APPLICATION DATA:
27     APPLICATION NUMBER: US/08/824,874
28     FILING DATE:
29     ATTORNEY/AGENT INFORMATION:
30     NAME: Billings, Lucy J.
31     REGISTRATION NUMBER: 36,749
32     REFERENCE/DOCKET NUMBER: PF-0252 US
33     TELECOMMUNICATION INFORMATION:
34     TELEPHONE: 415-855-0555
35     TELEFAX: 415-845-4166
36     INFORMATION FOR SEQ ID NO: 1:
37     SEQUENCE CHARACTERISTICS:
38     LENGTH: 268 amino acids
39     TYPE: amino acid
40     STRANDEDNESS: single
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QY	127	WGSTSPOLRLPHLRGANITIEHOKCENAYPGNIDITWCAVSEGGKNSCGDSDSGP	186
Db	165	WGTTKSPVHPFKVYLQCNISVLSQKRCEDAYPRQIDITMCAQ-DKAGRSDSCGDSGGP	223
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RESULT 10
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: Sequence 4, Application US/08790137
: Patent No. 5840871
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Goli, Suyu K.
: TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCI
: TITLE OF INVENTION: KALLIKREIN
: NUMBER OF SEQUENCES: 4
: CROSSREFERENCE ADDRESS:
: ADDRESSSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/790,137
: FILING DATE: Filed Herewith
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0195 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 263 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: GenBank
: CLONE: 55527
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[illegible]

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 23, 2002, 14:22:47 ; Search time 3129 Seconds

(without alignments)
2139.228 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0
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Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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10	1263	100.0	1204	6 AX491100	AX491100 Sequence
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DEFINITION Sequence 1 from Patent WO949055.
ACCESSION AX016287
VERSION AX016287.1 GI:10041854
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Bruck,C.E., Coche,T., Cassart,J.P. and Vinals-Bassols,C.
TITLE Human casb12 polypeptide, a serine protease
JOURNAL Patent: WO 949055-A 1 30-SEP-1999;
BRUCK CLAUDELINE ELVIRE MARIE (BE); SMITHKLINE BEECHAM BIOLOG (BE);
COCHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTA
(BE)
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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DEFINITION Sequence 3 from Patent WO949055.
ACCESSION AX016289
VERSION AX016289.1 GI:10041855
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Bruck,C.E., Coche,T., Cassart,J.P. and Vinals-Bassols,C.
TITLE Human casb12 polypeptide, a serine protease
JOURNAL Patent: WO 949055-A 3 30-SEP-1999;
BRUCK CLAUDELINE ELVIRE MARIE (BE); SMITHKLINE BEECHAM BIOLOG (BE);
COCHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTA
(BE)
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DB 721 GGTAGCTCCGGGGGCCCTGTGCTGTGAACCACTCTCTCAAGGCAATATCTCTCTGGGCG 780

OY 201 GlnAspProCysAlaIleThrArgLysProGlyValTyThrLysValCysLysTryVal 220
|||
DB 781 CAGATCGCTGTGGATCACCCGAAAGCCGTGGTGTCTACACGAAAGTGTGCAATATGTGTG 840

OY 221 AspTrpIleGlnGlnThrMetLysAsnAsn 230
|||
DB 841 GACTGATCCAGAGACGATGAAGAACAT 870

RESULT 4

LOCUS AB012917 1186 bp mRNA linear PRI 30-SEP-1998

DEFINITION Homo sapiens mRNA for serine protease (TLSP), complete cds.

VERSION AB012917.1 GI:3649790

KEYWORDS TLSP: serine protease (TLSP).

SOURCE Homo sapiens cDNA to mRNA.

ORGANISM Homo sapiens

REFERENCE 1 (sites)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Yoshida,S., Taniguchi,M., Suemoto,T., Oka,T., He,X. and Shiosaka,S.
cDNA cloning and expression of a novel serine protease, TLSP
JOURNAL Biochim. Biophys. Acta 1399 (2-3), 225-228 (1998)

MEDLINE 98438738

REFERENCE 2 (bases 1 to 1186)
Yoshida,S.
Direct Submission
Submitted (10-APR-1998) Shigetaka Yoshida, Nara Institute of
Science and Technology, Department of Structural Cell Biology,
Takayama 8916-5, Ikoma, Nara 630-0101, Japan
(E-mail:syoshide@s.ais-t-nara.ac.jp, Tel:81-743-72-5411,
Fax:81-743-72-5419)

JOURNAL


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Db 647 AACATCAGACACCATGCTGTGCGCAGCTGCAGAAAGGGGCGAAGCATCTCTGCAG 706
QY 181 GYASPSERGLYGLYPROLEUVALCYASNGINSEIRLEUNGINGLYILEISERTIPOLY 200
Db 707 GGTACTCCGGGGGCGCTCTGTGTGTACCAAGCTCTTCAAGGCATTATCTCTGGGGC 766
QY 201 GINASPPROCYSAIAIIEHRARGLYSPROGLYVALTYRTHLYSVALCYLSYSTYRVAL 220
Db 767 CAGATCCGTTGGTGGATCACCAGCAAGCTGTGTCTACAGAAAGTCTGCAATATGTG 826
QY 221 ASPTPILEGINGIUTHRMETLYSASN 230
Db 827 GACTGATCCAGAGACATGAACAAT 856

RESULT 6
AX358932 1204 bp DNA linear PAT 13-FEB-2002
LOCUS Sequence 185 from Patent WO0193983.
ACCESSION AX358932
VERSION AX358932.1 GI:18675367
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Baker,K.P., Desnoyers,L., Gerltsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smth,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0193983-A 185 13-DEC-2001;
Genentech Inc. (US)
FEATURES
source location/Qualifiers
1..1204
/organism="Homo sapiens"
/db-xref="taxon:9606"
BASE COUNT 306 a 364 c 294 g 240 t
ORIGIN
US-09-856-320a-2_COPY_53_282 (1-230) x AX358932 (1-1204)

Alignment Scores:
Pred. No.: 2.45e-97 Length: 1204
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x AX358932 (1-1204)
QY 1 ArgIleIleLysGlyPheGluCysLysProHisSerGlnProTyrPgiAlaIleLeuPhe 20
Db 166 AGGATCTATCAAGGGGTTCGAGTGCAGACCTTCACCTCCAGCCCTGGCAGGCCCTTTC 225
QY 21 GlnUlySthraTgLeuLeuCySgLyAlaThrLeuIleAlaProArgTyrPLeuThrAla 40
Db 226 GAGAAAGACGGGGCTACTCTGTGGGGCAGCGCTATCGCCCAAGATGGCTCTCAGACA 285
QY 41 AlaHisCysLeuLysProAlaGlyTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
Db 286 GCCCAGCTCTCAAGCCGCCCTACATAGTTCACCTGGGGGAGCAACCTCCCAAGAGAG 345
QY 61 GlnUlyCysGlnGlnThrArgTyrAlaThrGluSerPheProHisProGlyPheAsnAsn 80
Db 346 GAGGGCTGTGAGCAGACCCGGACAGCCATGAGTCTTCCGCCACCCGGCTTCAAGAAC 405
QY 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
Db 406 AGCCTCCCAACAAAGACACCGCATGACATCATGCTGTGGAAAGATGGCATGGCCAGTC 465
QY 101 SerLeuThrPheAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
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Db 466 TCCATCAGCTGGGGTGTGCGACCCCTCCTCTCCATCAGCTGTGCTGCTGCAGC 525
QY 121 SerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
Db 526 AGTGCCTCATTTCCGGCTGGGGGACAGACGTCACAGCCCCCGATTACGCTCTCTCACAC 585
QY 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGly 160
Db 586 TTGGCATGGCCCAACATCACCATTGATGACAGCAGAAAGTGTGAAACCGCTACCCGGC 645
QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
Db 646 AACATCAGACACCATGCTGTGCGCAGCTGCAGAAAGGGGCGAAGCATCTCTGCAG 705
QY 181 GYASPSERGLYGLYPROLEUVALCYASNGINSEIRLEUNGINGLYILEISERTIPOLY 200
Db 706 GGTACTCCGGGGGCGCTCTGTGTGTACCAAGCTCTTCAAGGCATTATCTCTGGGGC 765
QY 201 GINASPPROCYSAIAIIEHRARGLYSPROGLYVALTYRTHLYSVALCYLSYSTYRVAL 220
Db 766 CAGATCCGTTGGTGGATCACCAGCAAGCTGTGTCTACAGAAAGTCTGCAATATGTG 825
QY 221 ASPTPILEGINGIUTHRMETLYSASN 230
Db 826 GACTGATCCAGAGACATGAACAAT 855

RESULT 7
AX362425 1204 bp DNA linear PAT 15-FEB-2002
LOCUS Sequence 185 from Patent WO0208288.
ACCESSION AX362425
VERSION AX362425.1 GI:18694670
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Baker,K.P., Desnoyers,L., Gerltsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smth,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0208288-A 185 31-JAN-2002;
Genentech, Inc. (US)
FEATURES
source location/Qualifiers
1..1204
/organism="Homo sapiens"
/db-xref="taxon:9606"
BASE COUNT 306 a 364 c 294 g 240 t
ORIGIN
US-09-856-320a-2_COPY_53_282 (1-230) x AX362425 (1-1204)

Alignment Scores:
Pred. No.: 2.45e-97 Length: 1204
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x AX362425 (1-1204)
QY 1 ArgIleIleLysGlyPheGluCysLysProHisSerGlnProTyrPgiAlaIleLeuPhe 20
Db 166 AGGATCTATCAAGGGGTTCGAGTGCAGACCTTCACCTCCAGCCCTGGCAGGCCCTTTC 225
QY 21 GlnUlySthraTgLeuLeuCySgLyAlaThrLeuIleAlaProArgTyrPLeuThrAla 40
Db 226 GAGAAAGACGGGGCTACTCTGTGGGGCAGCGCTATCGCCCAAGATGGCTCTCAGACA 285
QY 41 AlaHisCysLeuLysProAlaGlyTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
Db 286 GCCCAGCTCTCAAGCCGCCCTACATAGTTCACCTGGGGGAGCAACCTCCCAAGAGAG 345
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QY	61	GlucylCysGlnGluThrThrGlyAlaThrGluSerPheProHisProGlyIleAsnAn	80		
QY	61	GlucylCysGlnGluThrThrGlyAlaThrGluSerPheProHisProGlyIleAsnAn	80		
Db	346	GAGGGCTGTGACACACACCCGGACACGACTGAGTCTTCCCCACCCGGCTTCAACAC	405		
QY	81	SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal	100		
Db	406	AGCCTCCCAACAAAGACACCGCATATGATCTGTTGAAAGATGGCATCGCAAGTC	465		
QY	101	SerIleThrThrPalaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr	120		
Db	466	TTCATTCACCTGGGGCTGTGGACCCCTCACCCCTCTCTCTACGCTGTGTCTCTGGACCC	525		
QY	121	SerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThr	140		
Db	526	AGCTGCCTCATTTTCCGGCTGGGGGACACAGTCACGCCCCCAATTCAGCTGCTTACACCC	585		
QY	141	LeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGly	160		
Db	586	TTGCATATGGCCCAACATCACCATCTATTGAGCACACGAAAGTGTGAGAAACGCTTACCCGGAC	645		
QY	161	AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGln	180		
Db	646	AACATTCACAGACACCATGGTGTGTCTCCACCGCTGACGAGGAGGGGGAGGACATCCGCCAG	705		
QY	181	GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGly	200		
Db	706	GGTGACTCCGGGGGGCCCTCTGTGTCTGTAAACCATGCTCTTCAAGGCATATATCTCTGGGGC	765		
QY	201	GlnAspProCysAlaIleThrArgLysProGlyValIlyThrLysValCysLysTyrVal	220		
Db	766	CAGGATCCGTGTGTGCATCACCCGAAAGCCTGTGTCTACACGAAAGTCTGCAAAATATGTG	825		
QY	221	AspTyrIleGlnGluThrMetLysAsnGln	230		
Db	826	GACTGTATCCAGAGACGATGAGAACAT	855		
RESULT 8	AX454622	1204 bp	DNA	linear	PAT 06-JUL-2002
LOCUS	AX454622				
DEFINITION	Sequence 207 from Patent WO0208284.				
ACCESSION	AX454622				
VERSION	AX454622.1	GI:21713935			
KEYWORDS					
SOURCE					
ORGANISM	human.				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE					
AUTHORS	1 Baker,K.P., Ferrara,N., Gerber,H., Gerlitsen,M.E., Goddard,A.,				
	Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,				
	Paoon,I.N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.				
	and Ye-W				
TITLE	Compositions and methods for the diagnosis and treatment of				
	disorders involving anglogenesis				
JOURNAL	Patent: WO 0208284-A 207 31-JAN-2002;				
	Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone				
	(US) ; Gerber, Hanspeter (US) ; Gerlitsen, Mary E. (US) ; Goddard,				
	Andrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;				
	Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)				
	; Paoon, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;				
	Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William				
	I. (US)				
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Pred. No.:	2.45e-97				1204
Score:	1263.00				230

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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DB	166	AGGATCATCAAGGGTTTGAGTGCACAAAGCTCACTCCAGCCCTGGCAGGACCCCTGTTC	225
QY	21	GluIyStrArGLeudCysGLyAlaThrIleuIleAlaProArgTrpLeuThrAla	40
DB	226	GAGAGAGCGGGCTACTGTGTGGGGCGAGCGCTCATCGCCGCCAGATGGCTCTGACAGCA	285
QY	41	AlaHIScYsLeuLYSProArgTrpIleValHISLeuGLyGlnHISAsnLeuIlnySgu	60
DB	286	GCCACTCTCTCAACCCCCGCTACTAGTTCACCTGGGGCACACAACTCCAGAAAGG	345
QY	61	GlulIyCySGluGlnThrArqThrAlaThrIuSerPheProHISProGLyPheAsnSn	80
DB	346	GAGGCTGTGAGACAGCCCGGACAGCCACTAGTGTCTTCCCCACCCGGCTTCAACAC	405
QY	81	SerLeuProAsnLYSAspHISArgAsnApIleMetLeuValLYSMetAlaSerProVal	100
DB	406	AGCCCTCCCAACMAAGACACCGCATATACATCAAGCTGGTGMAATGATGCATCGCCAGTC	465
QY	101	SerIleThrTrpAlaValArgProLeuThrIleuSerSerArgCysValThrAlaGlyThr	120
DB	466	TCCATCACCTGGGGCTGTGGAGCCCTCAACCTCTCTCAAGCTGTGTCTACTCTGGCAC	525
QY	121	SerCysLeuIleSerGLyTrpGLySerThrSerSerProGlnLeuArgLeuProHISthr	140
DB	526	AGCTGCTCATTTTCCGGCTGGGGCGACAGCTCCACGCCCACTTACGCTCGCTCACACC	585
QY	141	LeuArgCysAlaAsnIleThrIleIleGlnHISGlnLYSCysGluAsnAlaLeuTrpProGLy	160
DB	586	TTGCGATCGCCACACATCAACCTCACTTAAGCACCAAGAGTGGAAACAGGGCTTACCCCGGC	645
QY	161	AsnIleThrAspThrMetValCysAlaSerValGlnGluGLyLYSAspSerCysGln	180
DB	646	AACATCACAGACACCATGTGTGTCCAGCGTGCAGAAAGGGGGCAAGAGCTCGGGCAG	705
QY	181	GlyaspSerGLyGLyProLeuValCysAsnGlnSerLeuGlnGLyIleIleSerTrpGLy	200
DB	706	GGTGATCTCGGGGGGCCCTGTGTGTAAACAGTCTCTTCAAGGCATTAATCTCCGTGGGGC	765
QY	201	GlnAspProCysAlaIleThrArqTrpProGLyValLYrThrLYSValCysIlyStrVal	220
DB	766	CAGATCCGTGTGCATCAACCGAAAGCTGTGTCTACAGAAAGTCTGCCAAATATGTG	825
QY	221	AspTrpIleGlnGluThrMetLYSAsnSn	230
DB	826	GACTGTATCCAGAGACGATGAAGAACAT	855

RESULT 9	AX464372	1204 bp	DNA	linear	PAT 16-JUL-2002
LOCUS	AX464372				
DEFINITION	Sequence 505 from Patent WO0140466.				
ACCESSION	AX464372				
VERSION	AX464372.1				
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
	1				
	Baker,K.P., Beresini,M., DeForge,L., Desnoyers,L., Filvaroff,E.,				
	Geo,W.O., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,				
	Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,				
	Wood,W.L. and Zhang,Z.				
	Secreted and transmembrane polypeptides and nucleic acids encoding				
	same				

Db 766 CAGATCCGTCGTGGATCACCAGCCGAGCTGCTACAGAAAGTCTGCAATATGTG 825

QY 221 AsPTriplegInjurMetLysAsn 230
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 Db 826 GACTGATCCAGAGACGATGAACAAT 855

RESULT 11
 BC022068

LOCUS BC022068 1213 bp mRNA linear PRI 24-JAN-2002
 DEFINITION Homo sapiens, kallikrein 11, clone MGC:33060 IMAGE:4824387, mRNA,
 complete cds.

ACCESSION BC022068
 VERSION BC022068.1 GI:18314497
 KEYWORDS MGC.

SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1213)

REFERENCE 1
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (22-JAN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
 USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 CONTACT MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
 Toshynki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadan@systemsbiology.org
 Anup Madan, Jessica Fahy, Erin Heltton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whitting

FEATURES
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BASE COUNT 290 a 376 c 296 g 251 t

ORIGIN

Alignment Scores:
 Pred. No.: 2,47e-97 Length: 1213
 Score: 1263.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x BC022068 (1-1213)

QY 1 ArgLlelleysglypnehlucyslserProHisSerGlnProTrpGlnAlaLeuPhe 20
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Db 193 AGGATCATCAAGGGGTTGAGTGTGCAAGCCCTCAGTCCAGGCCCTGGCAGGACGCTTTC 252

QY 21 GtLulThrArgLeuLeuCySGlyAlaThrLeuLeuLeuAlaProArgTrpLeuLeuAla 40
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Db 253 GAGAAAGAGCGGGCTACTCTGTGGGCGCAGCTCATGCCGCCAGAGNGGCTCTGACAGCA 312

QY 41 AlaHisCysLeuLysProArgTrpLleValHisLeuGlyGlnHisAsnLeuGlnLysGln 60
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Db 313 GCCACTGCTCTCAAGCCCGCTCATAGTTCACCTGGGAGGACAACTCCGAAAGAG 372

QY 61 GluGlyCysGluGlnThrArgTrpAlaThrGluSerPheProHisProGlyIleAsnAsn 80
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Db 373 GAGGGCTGTAGCAGACAGCCGCGACGACCATGATCTCTCCCGCCAGCCGCTTCACAC 432

QY 81 SerLeuProAsnLysAspHisArgAsnAspIleLeuLeuValLysMetAlaSerProVal 100
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Db 433 AGCTCCCAACAAAGACACACCCCAATGACATCATGCTGTGAAGATGGCATGCCAGTC 492

QY 101 SerLleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
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Db 493 TCCATCACTGGGCTGTGCGACCCCTCACCTCTCTCAGCTGTGTCACTGCTGGCACC 552

QY 121 SerCysLeuLleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisTrp 140
 |||||

Db 553 AGCTGCTCTATTTCCGGCTGGGCGAGCAGCTCCAGCCCCAGTACGCTGCTCACACC 612

QY 141 LeuArgCysAlaAsnLleThrLleLeuHisGlnLysCysGlnAsnAlaTrpProGly 160
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Db 613 TTGCGATGCCCAACATCATCATATGAGCAGACAGAGTGTGAAGCGCTACCCCGG 672

QY 161 AsnLleThrSphrMetValCysAlaSerValGlnGlyLysLysAspSerCysGln 180
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Db 673 AACATCACAGACACCATGGGTGTGCGAGCTCAGAGAGAGGGGCAAGGCTCTCCGAG 732

QY 181 GlyAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnLysLleLleSerTrpGly 200
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Db 733 GGGAGCTCGGGGGCCCTGTGCTGAACCAATCTCTTCACAGCATTTATCTCTGGGG 792

QY 201 GlnAspProCysAlaLleThrArgLysProGlyValTrpThrLysValCysLysTrpVal 220
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Db 793 CAGGATCCGTCGTGATCACCCGAAAGCCGTGTGTACAGAAAGTGTCAATATGTG 852

QY 221 AsPTriplegInjurMetLysAsn 230
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Db 853 GACTGATCCAGAGACGATGAACAAT 882

RESULT 12
 AB041036 1301 bp mRNA linear PRI 20-JUN-2000
 LOCUS AB041036
 DEFINITION Homo sapiens mRNA for prostate-type 11prostaticin, complete cds.
 ACCESSION AB041036
 VERSION AB041036.1 GI:8574438
 KEYWORDS prostate-type 11prostaticin.
 SOURCE Homo sapiens prostate cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (sites)

REFERENCE 1 (sites)
 AUTHORS Mitsui, S., Yamada, T., Okui, A., Koninami, K., Uemura, H. and
 Yamaguchi, N.
 TITLE A novel isoform of a kallikrein-like protease, TLSP/11prostaticin,
 (PKSS20), is expressed in the human brain and prostate
 Biochem. Biophys. Res. Commun. 272 (1), 205-211 (2000)
 MEDLINE 20329229
 REFERENCE 2 (bases 1 to 1301)
 AUTHORS Yamaguchi, N. and Mitsui, S.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAR-2000) Nozomi Yamaguchi, Kyoto Prefectural

University of Medicine, Res. Ins. Geriatrics, Kawamachi Hirokoji,
Kyoto, Kyoto 602-8566, Japan (E-mail: nozomilekoto.kpu-m.ac.jp,
Tel:81-75-251-5848, Fax:81-75-251-5848)

FEATURES

source

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LLTSRCVTAGTSLTISMGSTSPOLRLPTLLCAATTIEHCKENAYPGNTIDM
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BASE COUNT

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Alignment Scores:

Pred. No.: 2,67e-97 Length: 1301
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 1 Argilellelysglypnehlucylslyspromisserginprotrpglnalalauphe 20
Db 269 AGGATCATCAAGGGGTGAGTGCAGAGCTCCTCCAGCCCTGGCAGGAGCCCTGTC 328
QY 21 Gluysrthraaglleucysglyalathrleuilealaproagtrpleuethr 40
Db 329 GAGAGAGCGCGCTACTGTGGGGCGAGCTCATCGCCCGAGATGGCTCTGCACACA 388
QY 41 Alanhsycsleuysproargtrylevalhlsleuglylnhisasnleuglnysglu 60
Db 389 GCCCACTCCTCAAGCCCCGCTACCTAGTCACTGGGGCGAGCACACCTCCAGAGAG 448
QY 61 Gluylcysgluglnthrargthralthrghuserpheprohispoglypheasn 80
Db 449 GAGGCTGTGAGCAGACCCGAGACCCACTGAGTCTCCCGCCAGCCGGCTTCAACAC 508
QY 81 Serleuproasnlyasphsargasnasprilemetleuvalysmetalseserprova 100
Db 509 AGCTCCCAACAAAGACACCGGACATGATGCTGTGAAGATGGCATCGGCACTC 568
QY 101 Serlethrtrpalaalargproleuthrleuserserargcysvalthr 120
Db 569 TCCATACACTGGGCTGTGGAGCCCTCCTCCTCCTGCTGCTACCTGCTGGCACC 628
QY 121 Serlysleuileserglytrpglyserthrserserproglinleuargleuprohis 140
Db 629 AGCTGCCCATTTCCGGCTGGGGGAGCAGCTCCAGCCCGGATTACGCTCCTCACACC 688
QY 141 Leuargcysalaasnlethrillelleglnhsglnyscysgluasnalaityprogly 160
Db 669 TTGGGATGGCGCAACATCATCATTTAGCAGCAGAAAGTGTGAAGAGCTTACCCGGC 748
QY 161 Asnlethrthraapthrmelvalcysalaservalglnuglyglylyaspserser 180
Db 749 AACATCAACAGACACCATGTGTGTGCCAGCTGCAGGAAGGGGGGAGAGATCTCTGGCAG 808
QY 181 Glylspserglyglyproleuvalcysanglnserleuglnlyllelsertrp 200
Db 809 GGTACTCTCGGGGGCCCTCTGTGTGAACAGTCTTCAAGGACATATATCTCTGGGGC 868
QY 201 Glnasprocyalaalathrarglyspoglyvaltyrthrlyvalcylslystyrval 220

Db 869 CAGGATCCGTGTGCATATACCCGAAAGCCTGTGTCTACAGAAAGTGTGAAAATATGTG 928
QY 221 Asprtrpilleglnthrmetlysasn 230
Db 929 GACTGTGATCCAGAGACCATGAGAACAAAT 958

RESULT 13

AR098430

LOCUS

AR098430

1314 bp

DNA

linear

PAT 14-FEB-2001

DEFINITION Sequence 2 from patent US 6075136.

ACCESSION

AR098430

VERSION

AR098430.1

GI:12807687

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 1314)

AUTHORS

Tang,Y.Tom., Corley,N.C. and Guejler,K.J.

TITLE

Prostate-associated serine protease

JOURNAL

Patent: US 6075136-A 2 13-JUN-2000;

FEATURES

Location/Qualifiers

1..1314

BASE COUNT

320 a

400 c

337 g

257 t

Alignment Scores:

Pred. No.: 2,7e-97 Length: 1314
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x AR098430 (1-1314)

QY 1 Argilellelysglypnehlucylslyspromisserginprotrpglnalalauphe 20
Db 284 AGGATCATCAAGGGGTGAGTGCAGAGCTCCTCCAGCCCTGGCAGGAGCCCTGTC 343
QY 21 Gluysrthraaglleucysglyalathrleuilealaproagtrpleuethr 40
Db 344 GAGAGAGCGCGCTACTGTGGGGCGAGCTCATCGCCCGAGATGGCTCTGCACACA 403
QY 41 Alanhsycsleuysproargtrylevalhlsleuglylnhisasnleuglnysglu 60
Db 404 GCCCACTCCTCAAGCCCCGCTACCTAGTCACTGGGGCGAGCACACCTCCAGAGAG 463
QY 61 Gluylcysgluglnthrargthralthrghuserpheprohispoglypheasn 80
Db 464 GAGGCTGTGAGCAGACCCGAGACCCACTGAGTCTCCCGCCAGCCGGCTTCAACAC 523
QY 81 Serleuproasnlyasphsargasnasprilemetleuvalysmetalseserprova 100
Db 524 AGCTCCCAACAAAGACACCGGACATGATGCTGTGAAGATGGCATCGGCACTC 583
QY 101 Serlethrtrpalaalargproleuthrleuserserargcysvalthr 120
Db 584 TCCATACACTGGGCTGTGGAGCCCTCCTCCTCCTGCTGCTACCTGCTGGCACC 643
QY 121 Serlysleuileserglytrpglyserthrserserproglinleuargleuprohis 140
Db 644 AGCTGCCCATTTCCGGCTGGGGGAGCAGCTCCAGCCCGGATTACGCTCCTCACACC 703
QY 141 Leuargcysalaasnlethrillelleglnhsglnyscysgluasnalaityprogly 160
Db 704 TTGGGATGGCGCAACATCATCATTTAGCAGCAGAAAGTGTGAAGAGCTTACCCGGC 763
QY 161 Asnlethrthraapthrmelvalcysalaservalglnuglyglylyaspserser 180
Db 764 AACATCAACAGACACCATGTGTGTGCCAGCTGCAGGAAGGGGGGAGAGATCTCTGGCAG 823

QY	181	GIASPPROCYSA	LA	LE	THR	ARG	LYS	PRO	GLY	VAL	TYR	THR	LYS	VAL	CYS	LYS	TYR	VAL	220
Db	824	GGTGACTCCGGGGGGCCCTCTGCTCTGTACTAACCAAGTCTCTTCAAGGCATTATCTCCCTGGGGC																	883
QY	201	GIASPPROCYSA	LA	LE	THR	ARG	LYS	PRO	GLY	VAL	TYR	THR	LYS	VAL	CYS	LYS	TYR	VAL	220
Db	884	CAGGATCCGCTGTGCATCCCGAAGCCTGTGTCTACAGAAAGTCTGCAAAATATGTG																	943
QY	221	ASPTPLIEGLING	LU	THR	MET	LYS	ASN												230
Db	944	GACTGTATCCAGAGACGATGAAGAACAAT																	973
RESULT 14																			
LOCUS	ARI52173	ARI52173									1166	bp	DNA				linear		PAT 08-AUG-2001
DEFINITION	Sequence 7 from patent US 6232456.																		
ACCESSION	ARI52173																		
VERSION	ARI52173.1	GI:15118223																	
KEYWORDS																			
SOURCE	Unknown.																		
ORGANISM	Unknown.																		
REFERENCE	1 (bases 1 to 1166)																		
AUTHORS	Cohen, M., Colpitts, T.L., Friedman, P.N., Granados, E., Klaas, M.R., Russell, J.C., Stewart, R.D. and Strome, S.D.																		
TITLE	Series protease reagents and methods useful for detecting and treating diseases of the prostate																		
JOURNAL	Patent: US 6232456-A 7 15-MAY-2001;																		
FEATURES	Location/Qualifiers																		
source	1..1166																		
BASE COUNT	259 a 381 c 285 g 237 t																		4 others
ORIGIN																			
Alignment Scores:																			
Pred. No.:	2.43e-96																		1166
Score:	1251.00																		228
Percent Similarity:	99.13%																		
Best Local Similarity:	99.13%																		
Query Match:	99.05%																		
DB:	6																		0
US-09-856-320A-2_COPY_53_282 (1-230) x ARI52173 (1-1166)																			
QY	1	ArgIleIleIeLysGlyPheGluCysLysProHisSerGlnProTyrGlnAlaLeuPhe																	20
Db	163	AGGATCATCAAGGGGCTTGAGAGTCAGACGCTCCACGCTGCGAGGACACCTGCTTC																	222
QY	21	GIUvSTTRArGLeuLeuCYsGlyAlaThrLeuIleAlaProArgTyrLeuThrAla																	40
Db	223	RAGAAAGCGGGCTACTCTGTGGGCGAGCGCTCAATCGCCCGCCAGATGGCTCTCGACAGCA																	282
QY	41	AlaHisCysLeuLysProArgTyrTLeValHisLeuGlyGlnHisAsnLeuGlnLysGlu																	60
Db	283	GCCCACTGCTCAAGCCCCGCTACATATGTCACTCGGGGCAACACCTCCAGAA																	

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Db      583 TTGGCATGCGCCAAATCATTACCTATTTGTAGCACCGAAGTGTGAAGAAGCCCTACC CGGC   642
Oy      161 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGln   180
Db      643 AACATCACAGAACCATGTGTGTGCCAGCGTGCGAGAAAGGGGCGCAAGACTCTCCG CAG   702
Oy      181 GlysAspSerGlyValProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpPly   200
Db      703 GGTCGACTCGGGGGGGCCCTCTGTGTGTGAACCGCTCTTTCAGGCAATATCTCTCGGG GC   762
Oy      201 GlnAspProCysAlaIleThrArgLysProGlyValTyrrThrLysValCysLysTyrVal   220
Db      763 CAGGATCCGCTGTGGCATCACCGAAGAGCGCTGTGTCTACAGAAAGTCTGCAAAATAATGTG   822
Oy      221 AspTrpIleGlnGlnThrMetLysAsnAsn   230
Db      823 GACTGTATCCAGAGACGATGAAGAACAT   852

RESULT 15
AR060847 LOCUS AR060847 833 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5840871.
ACCESSION AR060847
VERSION AR060847.1 GI:5987297
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 833)
TITLE Hillman,J.L. and Goll,S.K.
JOURNAL Prostate-associated kallikrein
Patent: US 5840871-A 2 24-Nov-1998;
FEATURES Location/Qualifiers
Source 1..833
BASE COUNT 169 a 283 c 221 g 155 t 5 others
ORIGIN

Alignment Scores:
Pred. No.: 1.01e-93 Length: 833
Score: 1218.00 Matches: 220
Percent Similarity: 97.83% Conservative: 5
Best Local Similarity: 95.65% Mismatches: 5
Query Match: 96.44% Indels: 0
DB: 6 Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x AR060847 (1-833)
Oy      1 ArgIleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPhe   20
Db      96 CGGATTTGGGGAGGGGTGGGAGTGTGAGCAGCATTTCCAGCCCTGGCAGCGGCTGTAC   155
Oy      21 GluLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAla   40
Db      156 CAGAAAGACGGCGCTACTCTGTGGGGCGCAGTWCATMGCCCCCAGATGGTTCTGTACACA CA   215
Oy      41 AlaHisCysLeuLysProArgTyrTrlLeuHisIstLeuGlyGlnHisAsnLeuGlnLysGlu   60
Db      216 GCCCACTCCCTNMAAGCCCCCGCTACTTAATTTACCTGGGGGCGACCAACCTCCAGAAAGAG   275
Oy      61 GluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsn   80
Db      276 GAGGGCTGTGAGCAGACCCGGACAGCCCACTAGTCCTTCCCACCCCGGCTTCAACAC AC   335
Oy      81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal   100
Db      336 AGCCTCCCCCAAAGAACACCCGCAATACATCTATGTGGTGAAGATGCGATCCCACTC   395
Oy      101 SerIleThrTrpAlaValArgProLeuThrIleuSerArgCysValThrAlaGlyThr   120
Db      396 TCATACACCTGGGGCTGTAGCAGCCCTCACCCCTTCTCTACGCTGTGTACTGTGGCACC   455

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QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
|||||
Db 456 AGTGCCCTCATTTCCGGCTGGGCGAGCACGTCAGCCCCAGTTACGCTGCTCACACC 515
QY 141 LeuArgCysAlaAsnIleThrIleIleGlnIlyscysGluAsnAlaTyrProGly 160
|||||
Db 516 TTGGGATGGCCAAACATCACCATCTTGAAGCAGAGAGTGTGAGAAAGCCTACCCCGGC 575
QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlyGlyLysAspSerCysGln 180
|||||
Db 576 AACATCACAGACACCACATGCTGTGCCAGCGCTGCAGAGAGGGGCAAGGACTCCTGCCAG 635
QY 181 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 200
|||||
Db 636 GGTGACTCCGGGGGCCCTCTGTGTAAACAGTCTTCAAGGCATTATCTCCTGGGGC 695
QY 201 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 220
|||||
Db 696 CAGGATCCGTGTCCGATCACCCGAAAGCCTGTGTCTACACGAAAGTCTGCAAAATATGTG 755
QY 221 AspTrpIleGlnIleThrMetLysAsnAsn 230
|||||
Db 756 GACTGGATCCAGAGACGATGAGACACAT 785

Search completed: December 23, 2002, 16:02:33
Job time : 3136 secs

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; Sequence 284, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (145)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (147)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (148)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (185)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (201)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-898-284
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Query Match 56.9%; Score 719; DB 10; Length 247;
Best Local Similarity 57.2%; Pred. No. 3.6e-59;
Matches 131; Conservative 33; Mismatches 65; Indels 0; Gaps 0;
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QY 1 RIIGFECRHSOPWQALAEKTRLLCGATLLAPRWLLTAHCKPRYIVHLCOHNIQKE 60
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
Db 19 RAIGAECCRNQSPWQAGLHRLFCGATLLSDRWLLTAHCKPRYIVHLCOHNIQKE 78
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
QY 61 ECGEQTATSPHPGPNNSLPKNDHNDIMLVKASPVSTWAVRPLTSSRCVTAGT 120
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
Db 79 EGPEQLRVYDFPHPGFNKDLSDANDNDIMLRPRQARLSAVQPLNLSQTCVSPGM 138
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
QY 121 SCLISGSGTSSPOLRLPHRLRCANITIIHOKCENAYPGNITDVMCASVOEGKDSQ 180
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
Db 139 QCLISGSGXSSPRALRPVTLQCANISILENKLCHMAYPGHISDSMXCAGIMEGRGSCQ 198
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
QY 181 GDSGGLPVCNOSLOGIISMGODPCATIRKPGVYTKVCKYVDWIOETMKN 229
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
Db 199 GDXGGLPVCNGLAGVVGGAEPGSRPRRAVYTSVCHTIDWIOELMEN 247
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
```

```
RESULT 3
US-09-764-847-742
; Sequence 742, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 742
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
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; LOCATION: (145)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (147)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (148)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (185)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (201)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-847-742
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```
Query Match 56.9%; Score 719; DB 10; Length 247;
Best Local Similarity 57.2%; Pred. No. 3.6e-59;
Matches 131; Conservative 33; Mismatches 65; Indels 0; Gaps 0;
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QY 1 RIIGFECRHSOPWQALAEKTRLLCGATLLAPRWLLTAHCKPRYIVHLCOHNIQKE 60
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
Db 19 RAIGAECCRNQSPWQAGLHRLFCGATLLSDRWLLTAHCKPRYIVHLCOHNIQKE 78
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
QY 61 ECGEQTATSPHPGPNNSLPKNDHNDIMLVKASPVSTWAVRPLTSSRCVTAGT 120
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
Db 79 EGPEQLRVYDFPHPGFNKDLSDANDNDIMLRPRQARLSAVQPLNLSQTCVSPGM 138
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
QY 121 SCLISGSGTSSPOLRLPHRLRCANITIIHOKCENAYPGNITDVMCASVOEGKDSQ 180
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
Db 139 QCLISGSGXSSPRALRPVTLQCANISILENKLCHMAYPGHISDSMXCAGIMEGRGSCQ 198
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
QY 181 GDSGGLPVCNOSLOGIISMGODPCATIRKPGVYTKVCKYVDWIOETMKN 229
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
Db 199 GDXGGLPVCNGLAGVVGGAEPGSRPRRAVYTSVCHTIDWIOELMEN 247
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
```

```
RESULT 4
US-09-796-294-8
; Sequence 8, Application US/09796294
; Patent No. US20020037581A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Extracellular Serine Protease
; FILE REFERENCE: D6020CIP3
; CURRENT APPLICATION NUMBER: US/09/796,294
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/618,259
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 8
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of mouse neuropilin homologous
; OTHER INFORMATION: to TAD6-14; accession no. D30785
; US-09-796-294-8
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Query Match 54.3%; Score 686; DB 10; Length 260;
Best Local Similarity 52.8%; Pred. No. 4.3e-59;
Matches 121; Conservative 36; Mismatches 70; Indels 2; Gaps 2;
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QY 1 RIIGFECRHSOPWQALAEKTRLLCGATLLAPRWLLTAHCKPRYIVHLCOHNIQKE 60
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
Db 32 KLEGRRCIPHSQPMQALPQGERLGGVLDVDMVLTAAHCKKQKYSVRLDHSIQSR 91
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
QY 61 ECGEQTATSPHPGPNNSLPKNDHNDIMLVKASPVSTWAVRPLTSSRCVTAGT 120
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
Db 92 DPEQEOIYVNOSTIOHPCYNNSNP-EDHSBIDIMLRQNSANLGDVKYVOLANLCPKVGQ 150
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
QY 121 SCLISGSGTSSPOLRLPHRLRCANITIIHOKCENAYPGNITDVMCASVOEGKDSQ 180
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
```



```
Db 151 KCIISGCTVTSPOENFNPNTLNCAEVAKIYSQNCERATPGKITBGMVACG-SSNGADTCQ 209
QY 181 GDSGGPLVNCNQLGIIISWGODPCATRRKPGVYTKVKCYVDMIQETMRN 229
Db 210 GDSGGPLVCDGMLGIIISWGSDDPCGKPKPKPVYTKICHTYTMWIKTKTMN 258

RESULT 5
US-09-888-615-90
; Sequence 90, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHITE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERRARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888, 615
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-90

Query Match 54.2%; Score 684; DB 10; Length 320;
Best Local Similarity 51.7%; Pred. No. 8,4e-56;
Matches 124; Conservative 37; Mismatches 65; Indels 14; Gaps 3;

QY 1 RIIGFECKPHSQPWOAALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHLGCHNLQKE 60
Db 85 KILGDECAPHSQWQVVALYERGRFCGASLISPHWVLSAHCQSREYRVLGEHNLKR 144
QY 61 EGCQTRATSEFPHPGNNLSLPKNDHNDIMLYKMASPVITAVRPLTSSRCVYAGT 120
Db 145 DGPDLRTTSVYIPHYE---ARSHRNDIMLRLVQPAHLNPOVRPAVLPTRCPHPE 200
QY 121 SCLISGWTST-----SP--QLRLPHTLRCAITITIEHOKENAYPGNITDMVCAS 170
Db 201 ACVYSGMCLVSHNEPRGASPRSOVSLPDTLHCANISITISPTSCDKSTPGKLTIMVACG 260
QY 171 VOESGKDSQGDGSGPLVNCNQLGIIISWGODPCATRRKPGVYTKVKCYVDMIQETMRN 230
Db 261 AEGRGAESECDGSGPLVCGIIGIYVWGDVPCDNTTKPKGVYTKVCHYLEMIRETMKN 320

RESULT 6
US-09-978-295A-395
; Sequence 395, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
```

```
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978, 295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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Query Match 54.1%; Score 683; DB 9; Length 260;
Best Local Similarity 51.6%; Pred. No. 8e-56;
Matches 116; Conservative 43; Mismatches 64; Indels 2; Gaps 2;

QY 1 RIITGFECKRHSPQWQALFEKTRLLCGATLLPRLWTLTAHCLKPRYIYHLCOHNIQKE 60
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QY 61 ECGEORTATESFPHPFNSSLPNKDHRNDIMLVKASPVSTWAVRPLTSSRCVTAGT 120
DB 92 DGEQDELIVVQSLPHPCYNS-DVEDNHNHMLQLDLDOASLSKVPISLADHCTQPCQ 150
QY 121 SCLISGWSSTSPQLRPLHPLRCANITIEHOKCENAYPENGITDTWVCAVQEGGRDSCQ 180
DB 151 KCTVSGWGTYSRENPEPTLNCAYKIFQKCEADYPEQIIDGHWVCAVQEGGRDSCQ 209
QY 181 GDSGGLVCDGALQGITWSGSDPCGRSKGVYTNICRYLDMWIKK 225
DB 210 GDSGGLVCDGALQGITWSGSDPCGRSKGVYTNICRYLDMWIKK 254

RESULT 7
US-09-978-697-395
Sequence 395, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT FILING DATE: 2001-10-16
CURRENT FILING DATE: 2001-10-16
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Query Match 54.18; Score 683; DB 9; Length 260;
Best Local Similarity 51.68; Fred. No. 8e-56;
Matches 116; Conservative 43; Mismatches 64; Indels 2; Gaps 2;
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Db 92 DGEQELPVPVQSIDPHPCYNSS-DVEDHNHDLMLQLRDQASLSKVPFISLADHCTPGQ 150
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QY 181 GDSGGPLVCNQLGITSWGODPCATRRKPGVYTKVKCYDWIOE 225
Db 210 GDSGGPLVCAGLQGITISWGSDDPCGRSKDGVYITINICRIDWIKK 254
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RESULT 8
US-09-978-192A-395
Sequence 395, Application US/09978192A
Patent No. US2002017753A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc

;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
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;; APPLICANT: Gerber, Hanspeter
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC9
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6 PRIOR FILING DATE: 1998-04-30
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29 PRIOR APPLICATION NUMBER: 60/085338
30 PRIOR FILING DATE: 1998-05-13
31 PRIOR APPLICATION NUMBER: 60/085323
32 PRIOR FILING DATE: 1998-05-13
33 PRIOR APPLICATION NUMBER: 60/085582
34 PRIOR FILING DATE: 1998-05-15
35 PRIOR APPLICATION NUMBER: 60/085700
36 PRIOR FILING DATE: 1998-05-15
37 PRIOR APPLICATION NUMBER: 60/085689
38 PRIOR FILING DATE: 1998-05-15
39 PRIOR APPLICATION NUMBER: 60/085579
40 PRIOR FILING DATE: 1998-05-15
41 PRIOR APPLICATION NUMBER: 60/085580
42 PRIOR FILING DATE: 1998-05-15
43 PRIOR APPLICATION NUMBER: 60/085573
44 PRIOR FILING DATE: 1998-05-15
45 PRIOR APPLICATION NUMBER: 60/085704
46 PRIOR FILING DATE: 1998-05-15
47 PRIOR APPLICATION NUMBER: 60/085697

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RESULT 9
US-09-796-294-7
: Sequence 7, Application US/09796294
: Patent No. US20020037581A1

Query Match	51.4%	Score 649.5	DB 9	Length 293
Best Local Similarity	50.9%	Pred. No. 1.1e-52		
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OY	1	RIIKGFECRKHSPOQAA-LFEKTRLLCGATLIAPRWLLTAAHCLKPRYIVHLGONHLOK	59	
DB	66	RIINGSCDHTOPQOAAALLRPQOLCGAVLYHPOMLLTAAHCKRKVFRGLGHTSLP	125	
OY	60	-EEGCEQTRATESFPHRGFNNSLPNKDRNDMLVYMASPVSITMAVRPLTSSRCVTA	118	
DB	126	YVESGQMFQGVGSIPRGYS---HPGHSNDMLIKLNRIRPTKVDYRINVSHPESA	181	
OY	119	GTSCLLIGSMSTSSPOLRLHTLRKANITTEHCKENATPGNITTDIMWCAVSEGGRS	178	
DB	182	GTKCLVSGWGTSSPOVHFPRKVLQCLNIVSLSORCEDAYPRODDTMEFCAG-DKAGRDS	240	
OY	179	COGDSGAPLVNOSLOGIISMGODPCAITRRPGVYTVCKRVMDIOETMKN	230	
DB	241	COGDSGAPVVCNGLSLGSLVSKWDYPCAPRNPBGVYIMLCKFTKWIQETIOAN	292	
RESULT 11				
US-09-989-293a-309				
Sequence 309, Application US/09989293A				
Patent No. US20020177164A1				
GENERAL INFORMATION:				
APPLICANT: Ashkenazi, Avi J.				
APPLICANT: Baker, Kevin P.				
APPLICANT: Hotstein, David				
APPLICANT: Desnoyers, Luc				
APPLICANT: Eaton, Dan L.				
APPLICANT: Ferrara, Napoleone				
APPLICANT: Fong, Sherman				
APPLICANT: Gerber, Hanspeter				
APPLICANT: Gerritsen, Mary E.				
APPLICANT: Goddard, Audrey				
APPLICANT: Godowski, Paul J.				
APPLICANT: Grimaldi, J. Christopher				
APPLICANT: Gurney, Austin L.				
APPLICANT: Kljavin, Ivar J.				
APPLICANT: Napier, Mary A.				
APPLICANT: Pan, James				
APPLICANT: Paoni, Nicholas F.				
APPLICANT: Roy, Margaret Ann				
APPLICANT: Stewart, Timothy A.				
APPLICANT: Tumas, Daniel				
APPLICANT: Watanabe, Colin K.				
APPLICANT: Williams, P. Mickey				
APPLICANT: Wood, William I.				
APPLICANT: Zhang, Zemin				

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: p2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 60/090678
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PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694

RESULT 14
US-09-989-722-309
Sequence 309, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 51.4%; Score 649.5; DB 10; Length 293;

Best Local Similarity 50.9%; Pred. No. 1,1e-52;

Matches 118; Conservative 40; Mismatches 67; Indels 7; Gaps 4;

QY 1 RIIRGECRKHSPQMAA-LEKTRRLGATLLAPRMLTAAHCLKPRYVTLGQHNLOK 59
DB 66 RIIRGSDCHHTOPMAALLRPRQLCYGAVLVHPQMLTAAHCRKRVFRRLGHYSLSL 125
QY 60 -EECCQTRATBSFPHRGFNLSLPKNDHRNDMLVMAFVSITTAVAVRPLTSSRCVTA 118
DB 126 VYESGQMGFOGVKSIPIHFGS----HGHSNDLMLIKILNRIRPTKDVPRPLNVSSHCPSA 181
QY 119 GTSCLLIGMSTSPOLRLPHTLRCANITIIIEHOKCENAVPGNTTDMVCAVQEGGKDS 178
DB 182 GTKCLVSGMGTTSPOVHFPRVLCILNIVLSQRKCDATPRQIDPTMFCAG-DKAGRDS 240

QY 179 CQGDGSGPVLNQSILGIIISMGODPCATRKPGVYTRKCVYDVIQETMKNN 230
DB 241 CQGDGSGPVLNQSILGIIISMGODPCATRKPGVYTRKCVYDVIQETMKNN 292

RESULT 15
US-09-989-723-309
Sequence 309, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C62
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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      PRIOR FILING DATE: 1998-07-01
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      PRIOR FILING DATE: 1998-07-02
      PRIOR APPLICATION NUMBER: 60/091978
      PRIOR FILING DATE: 1998-07-07
      PRIOR APPLICATION NUMBER: 60/091982
      PRIOR FILING DATE: 1998-07-07
      PRIOR APPLICATION NUMBER: 60/092182
      PRIOR FILING DATE: 1998-07-09
    }
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}

Query Match          51.4%; Score 649.5; DB 10; Length 293;
Match Local Similarity 50.9%; Pred. No. 1,le=52;
Matches 118; Conservatvity 40; Mismatches 67; Indels 7; Gaps 4

Oy      1 RINGFECKPSPQOAQ-LFEKFTLLGATLAPRMULTAHCCLKPRIVYLGHONLOK 59
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Oy      -EEGCEQRRTATSEPHAGCFNNSLPNNKHDRNDIMLVKMASPVSIITWAVPLTSSRCVYA 118
        | : ||||| : : | : ||||| : : | : ||||| : : | : ||||| : : |

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Db 126 VYESGQMFQGVKSIPHPGYS---HPGHSNDMLIKINRIRIPTKDVRLINSSHCPSA 181
QY 119 GTSCILISGWSSTSSPOLRLPHTLRCANITITIEHOKCENAYPGNITDTMVCASVOEGGRDS 178
Db 182 GTKCLVSGMGSTKSPQVHPFVLQCLNISVLSQKRCEDAYPRQIDDTMFCAG-DKAGRDS 240
QY 179 CQGDSSGPPLYCNOISLOGIISWGDPCAITRKPGYTKVCKYVDMIOETMKN 230
Db 241 CQGDSSGPPYVNCISLOGIISWGDYPCARPNNPGYTNICKFTKWIOETIOAN 292

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